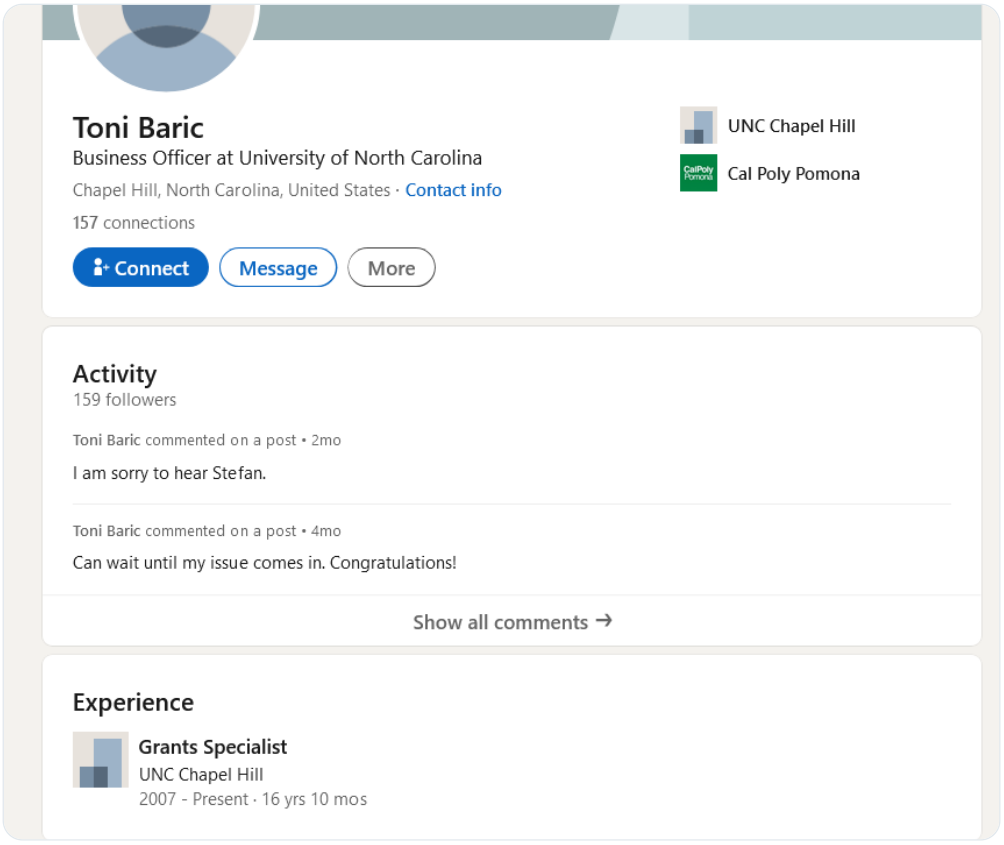
Destiny Rezendes @dezzie_rezzie

Oct 25, 2023 · 13 tweets · dezzie_rezzie/status/1716984766342279480

🧵1🔍 Who is Ralph Baric, really? We all know that he's the world's expert on coronaviruses & he is implicated in the lab leak 'theory' that resulted in the C19 pandemic, but do you REALLY know Baric & how important his role in C19 is?

2🧵In previous threads I have extensively looked into the career of Ralph Baric. Along the way I discovered that Baric's wife, Antoinette 'Toni' also works at UNC Chapel Hill as the school's Grant Specialist. Convenient.



3🧵When looking into this months ago I noticed Baric's CV listed his family member, which confirmed Antoinette Baric was indeed Ralph's wife. Also listed were two daughters [Cristina & Michelle], & two son's [Michael & Thomas]

Curriculum Vitae
Ralph S. Baric

I. PERSONAL INFORMATION:

A. Business Address:
Department of Epidemiology
School of Public Health
University of North Carolina at Chapel Hill
McGaveran-Greenberg Hall, CB# 7435
Chapel Hill, North Carolina 27599-7435
Phone: 919-966-3895

Home Address:
2600 Northstream Ct
Haw River, NC 27258
336-578-1575

B. Personal Data
Born: April 3, 1954
US Citizen

Married: Antoinette Baric
Children: Cristina, Michelle, Michael, Thomas

II. EDUCATION:

A. North Carolina State University, Raleigh, North Carolina, B.S., Zoology, 1977
B. North Carolina State University, Raleigh, North Carolina, Ph.D., Microbiology, 1983
C. University of Southern California, School of Medicine, Department of Microbiology and Neurology, Post-doctoral Fellow, 1982-1986

III. PROFESSIONAL EXPERIENCE:

A. Assistant Professor, Department of Parasitology and Laboratory Practice, University of North Carolina at Chapel Hill, March 1986-June 1990
B. Assistant Professor, Department of Epidemiology, University of North Carolina at Chapel Hill, July 1990-June 1993.
C. Associate Professor, Department of Epidemiology, University of North Carolina at Chapel Hill, July 1993-2001.
D. Associate Professor, Department of Microbiology and Immunology, University of North Carolina at Chapel Hill, July 1993-2001
E. Professor, Department of Epidemiology, Department of Microbiology and Immunology, University of North Carolina at Chapel Hill, July 2001-current

4🧵 In December of 2021, the NC regional Pulitzer-prize winning newspaper wrote a glowing article about Ralph Baric, announcing that he had just been given the highest civilian honor in the state by the governor. The article mentioned almost all aspects of Baric's life-almost..

Link: https://archive.ph/DQreQ

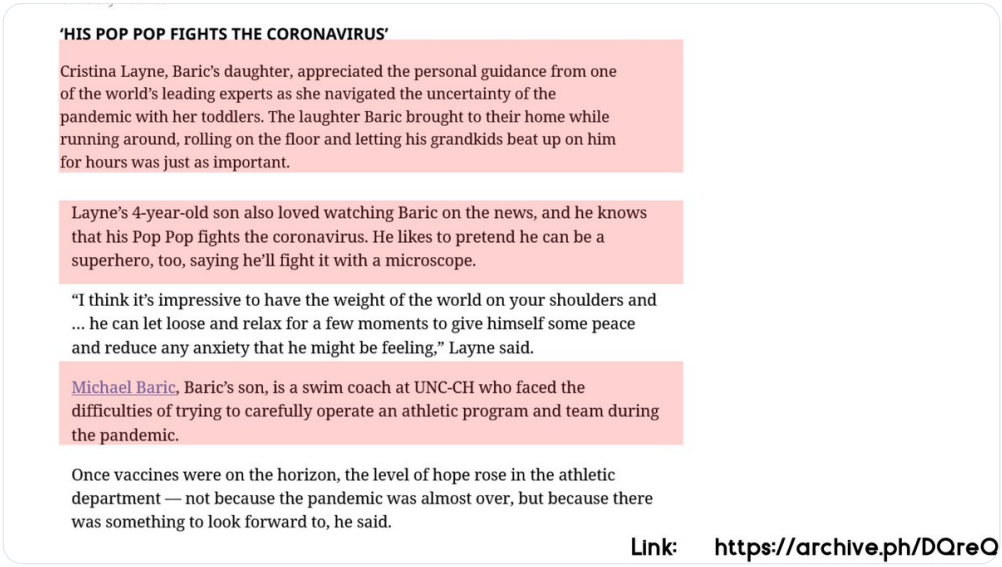
For his contributions to the development of the Moderna vaccine as well as Remdesivir and Molnupiravir, which are COVID-19 drug treatments, Baric is The News & Observer's 2021 Tar Heel of the Year. The distinction honors North Carolina residents who have made significant contributions to the state and region — and in this case, the world.

Dr. Ralph Baric, a scientist at UNC-Chapel Hill's Gillings School of Global Public Health, has studied coronaviruses for decades. Baric and researchers in his lab helped develop the Moderna vaccine and treatments for COVID-19 like Remdesevir. BY JULIA WALL

A COMMITMENT TO THE PROCESS

Baric's research was the basis for multiple vaccines, including Moderna, which was tested on animal models in his UNC-CH lab before it was given to people. His team also conducted the pre-clinical development for the only approved direct-acting antiviral drug, Remdesivir, to treat COVID-19 patients in hospitals. Baric's lab also studied Molnupiravir, which is the first antiviral pill shown to treat COVID-19 and was authorized for emergency use last month.

Link: https://archive.ph/DQreQ



'HIS POP POP FIGHTS THE CORONAVIRUS'

Cristina Layne, Baric's daughter, appreciated the personal guidance from one of the world's leading experts as she navigated the uncertainty of the pandemic with her toddlers. The laughter Baric brought to their home while running around, rolling on the floor and letting his grandkids beat up on him for hours was just as important.

Layne's 4-year-old son also loved watching Baric on the news, and he knows that his Pop Pop fights the coronavirus. He likes to pretend he can be a superhero, too, saying he'll fight it with a microscope.

"I think it's impressive to have the weight of the world on your shoulders and ... he can let loose and relax for a few moments to give himself some peace and reduce any anxiety that he might be feeling," Layne said.

Michael Baric, Baric's son, is a swim coach at UNC-CH who faced the difficulties of trying to carefully operate an athletic program and team during the pandemic.

Once vaccines were on the horizon, the level of hope rose in the athletic department — not because the pandemic was almost over, but because there was something to look forward to, he said.

Link: https://archive.ph/DQreQ

"It made me very proud, because I know he played a huge role in that," Michael Baric said.

For Toni, her husband brought a sense of relief during the pandemic and pride as she collected messages of gratitude from others.

One email came from a UNC-CH faculty member whose sister recovered from COVID-19 after being treated with Remdesevir. Another email was sent by a mom who thanked Baric for saving her son's life.

"The state and the country and the world are really lucky that Ralph did that, starting decades ago," said Johnston, a professor emeritus of microbiology and immunology at the UNC School of Medicine and the executive director of the nonprofit organization Global Vaccines Inc.

Link: https://archive.ph/DQreQ

5🧵 The article mentions his wife, Toni, their long history at UNC, their son, Michael who also works at UNC as a swim coach, their daughter, Cristina & even Baric's grandkids. No mention tho of Michelle & Thomas Baric. The other children...

In 2015, Baric and his colleagues at UNC-CH started working on Remdesevir, without knowing that in a few years it would be saving lives of patients at the hospital across the street and at those around the country. More than half of patients hospitalized with COVID-19 are given Remdesevir, according to biopharmaceutical company Gilead Sciences.

About two to three years before the COVID-19 pandemic, Baric and his colleagues started testing mRNA-based vaccines against other coronaviruses. The mRNA vaccines essentially teach cells how to make a protein that triggers an immune response that attacks the virus. Scientists like Baric have been pioneering that technology since the 1990s.

Their data was "spectacular" in animal models of human disease in how it could neutralize the virus through immune responses and protect young and old animals from lethal disease, Baric said. That data was rolling out just as SARS CoV-2 emerged, so Baric and other scientists used it as the foundation to develop vaccines to fight COVID-19.

Link: https://archive.ph/DQreQ

In collaboration with the NIH, Baric's lab was charged with developing similar animal models to test vaccine candidates by April 2020 and gather data by the end of June 2020, so it could be sent to the FDA to get approval for Phase 3 testing in humans, which began in August 2020.

"That trusting relationship and their expertise in animal model development allowed for early understanding of how efficacious COVID-19 vaccines were and undoubtedly led to the record speed of development," Corbett said.

She is an assistant professor of immunology and infectious diseases at Harvard University who worked with Baric while earning her doctorate at UNC-CH. Corbett helped develop the Moderna vaccine as a research fellow at the National Institute of Allergy and Infectious Diseases' Vaccine Research Center.

Graham, former deputy director of the NIAID Research Center at NIH, called Baric "the premier coronavirologist in the world.

Link: https://archive.ph/DQreQ

PREPARING FOR THE NEXT OUTBREAK

While Baric and his team have hit remarkable milestones throughout the pandemic, the celebratory moments have been fleeting.

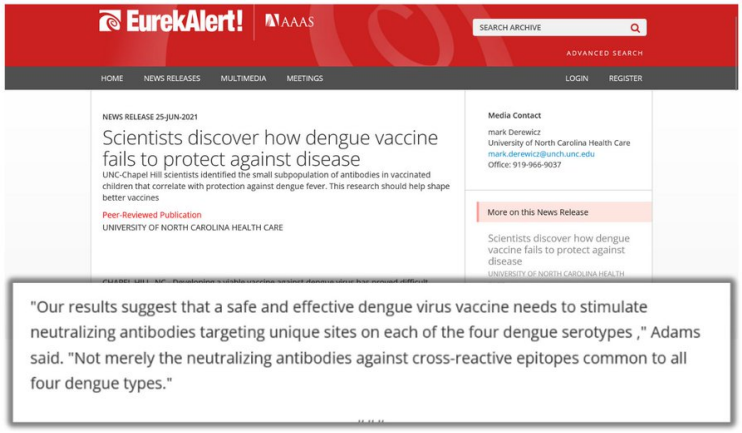
The day before a U.S. Food and Drug Administration panel gave preliminary approval to Molnupiravir in November, the omicron variant emerged. Baric's lab geared up to respond to that variant to understand its biology, its impact on therapeutics, vaccines and drugs, and how best to counter it if some of the products that are on a shelf lose their potency, Baric explained.

Accomplishments: Inducted into the National Academy of Sciences in 2021; UNC System O. Max Gardner Award in 2021; North Carolina Award in 2020.

Fun fact: Before the pandemic, Baric and his wife would eat lunch together nearly every day at UNC-Chapel Hill. Sometimes they would invite their son, Michael, who also works at UNC.

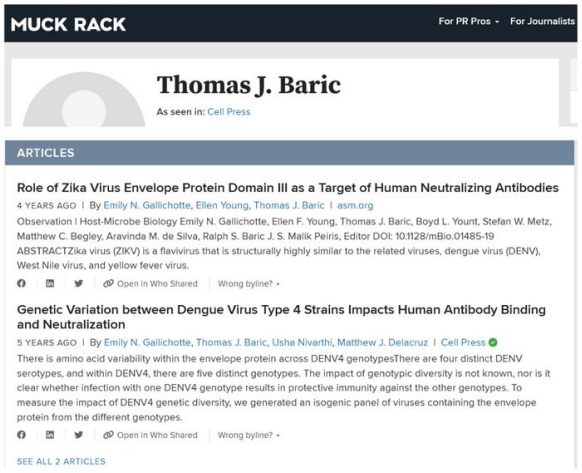
Link: https://archive.ph/DQreQ

6🧵 I found this very odd. Not only was Thomas Baric missing from the article, but also from Baric's CV. It took some digging but lo' & behold, Thomas Baric ALSO works at UNC, in fact he's on his way to follow his dad's footsteps; working on viruses/vaccines!



Link: https://www.eurekalert.org/news-releases/903503

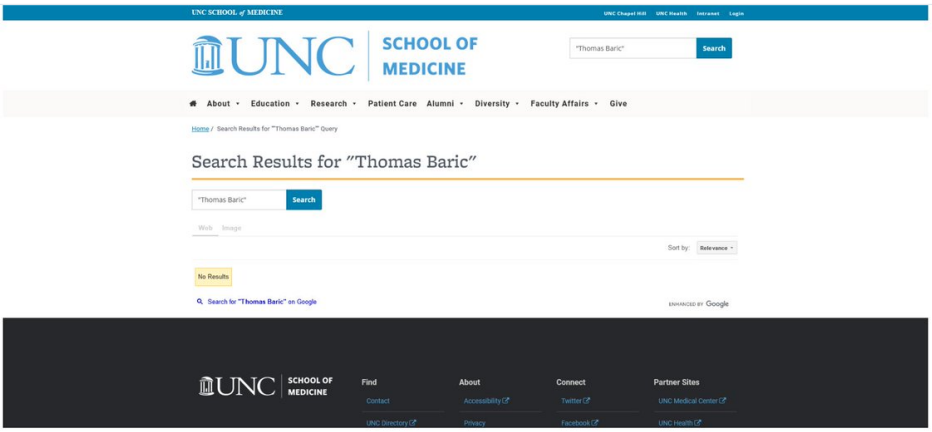
Link: https://journals.asm.org/doi/10.1128/mbio.01485-19



Link: https://muckrack.com/thomas-j-baric

Link: https://reporter.nih.gov/search/0vwNTqyItkC2pzco-LJNSA/project-details/9153244

7🧵Thomas Baric is listed as a scientist and co-author of multiple papers with his father Ralph working on the same studies that Ralph had been working on leading up to the pandemic including federally funded work. However, you don't find him if you search UNC's website. 🤔



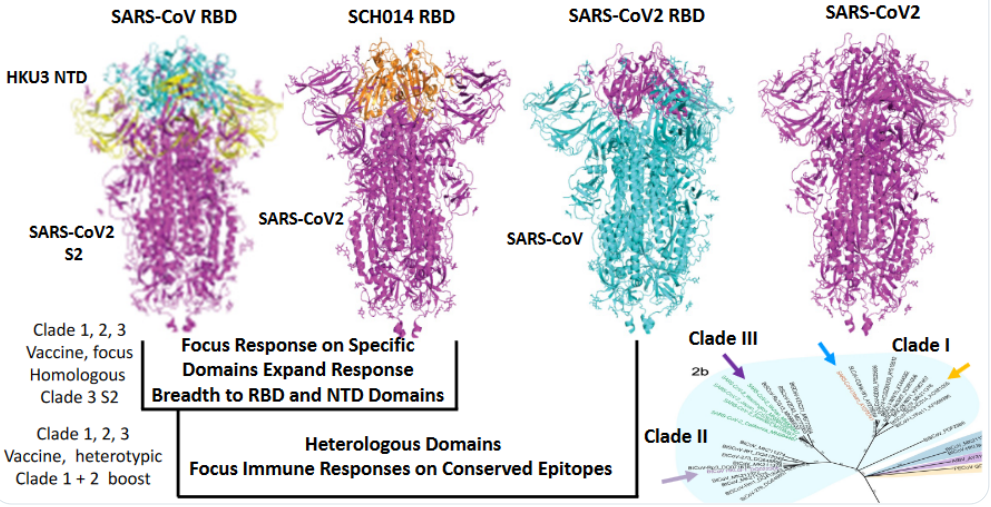
Link: https://www.med.unc.edu/?s=%22Thomas+Baric%22&cx=017059784719810698204%3Alj2ibo0i4wo&cof=FORID%3A10&ie=UTF-8&search-btn=Search&search_type=gcs#gsc.tab=0&gsc.q=%22Thomas%20Baric%22&gsc.page=1

8🧵I only found out due to a March 2022 WHO consultation document by UNC Chapel Hill titled, Major challenges w/the development of Pan-Coronavirus Vaccines, where on the last page is listed "Tommy Baric" & Acknowledged is Pfizer, Merck, Zuckerberg, & NIAID.

Common Obstacles

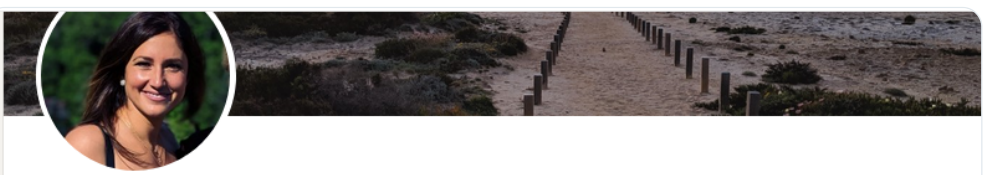
- **Sarbecoviruses**
  - Group II and Group III strains and assays
  - More High Risk Strains
- **Other Betacoronaviruses-**
  - MERS-CoV (group 2c)
    - heterologous group 2c high-risk strains/models
  - Group 2d strains (to be identified and developed)
  - Group 2a (HCoV OC43/HKU1)
    - limited reagents/animal models
    - lots of animal strains (surrogates)
- **Other Alphacoronaviruses**
  - NL63 and HCoV229E animal models (weak/nonexistent)
  - High Priority Zoonotic Strains (to be identified and developed)
    - Several animal strains/models available
- **Deltacoronaviruses**
  - Porcine epidemic diarrhea virus
  - Other high priority strains (to be identified and developed)

Chimeric Sarbecovirus Spike Vaccines



9🧵 Seems like Thomas wasn't forgotten from the article of his father's success. He was intentionally not mentioned. The big question is why? But the curiosity doesn't end there. Why nothing more than a mention of Michelle Baric?

10.🧵 Maybe it has something to do with the fact that Michelle works at Myriad Genetics [MG] Why is this relevant. Baric wasn't alone in his honors by the state of NC, another recipient was NIH director Francis Collins, another NC native.



Michelle Baric

Genetic Counselor at Myriad Genetics

Wrightsville Beach, North Carolina, United States · Contact info

185 connections

Connect | Message | More

Myriad Genetics

University of Cincinnati

Activity

184 followers

Michelle hasn't posted yet

Recent posts Michelle shares will be displayed here.

Show all activity →

Experience

Genetic Counselor

Myriad Genetics · Full-time

Aug 2020 - Present · 3 yrs 3 mos

Patient Education Team

Genetic Counselor

Duke University Health System · Full-time

Nov 2015 - Jul 2020 · 4 yrs 9 mos

Durham, NC

Francis Collins

31 languages

Article Talk | Read Edit View history Tools

From Wikipedia, the free encyclopedia

For other people named Francis Collins, see Francis Collins (disambiguation).

Francis Sellers Collins ForMemRS (born April 14, 1950) is an American physician-geneticist who discovered the genes associated with a number of diseases and led the Human Genome Project. He served as director of the National Institutes of Health (NIH) in Bethesda, Maryland, from 17 August 2009 to 19 December 2021, serving under three presidents.[1][2]

Before being appointed director of the NIH, Collins led the Human Genome Project and other genomics research initiatives as director of the National Human Genome Research Institute (NHGRI), one of the 27 institutes and centers at NIH. Before joining NHGRI, he earned a reputation as a gene hunter at the University of Michigan.[3] He has been elected to the Institute of Medicine and the National Academy of Sciences, and has received the Presidential Medal of Freedom and the National Medal of Science.

Collins also has written books on science, medicine, and religion, including the *New York Times* bestseller, *The Language of God: A Scientist Presents Evidence for Belief*. After leaving the directorship of NHGRI and before becoming director of the NIH, he founded and served as president of The BioLogos Foundation, which promotes discourse on the relationship between science and religion and advocates the perspective that belief in Christianity can be reconciled with acceptance of evolution and science, especially through the idea that the Creator brought about his plan through the processes of evolution.[4] In 2009, Pope Benedict XVI appointed Collins to the Pontifical Academy of Sciences.[5]

On October 5, 2021, Collins announced that he would resign as NIH director by the end of the year.[6] Four months later in February 2022, he joined the Cabinet of Joe Biden as Acting Science Advisor to the President, replacing Eric Lander.[7][8]

Early years [edit]

Collins was born in Staunton, Virginia, the youngest of four sons of Fletcher Collins and Margaret James Collins. Raised on a small farm in Virginia's Shenandoah Valley, Collins was home schooled until the sixth grade.[9] He attended Robert E. Lee High School in Staunton,

Francis Collins

Science Advisor to the President
Acting
In office
February 18, 2022 – October 3, 2022

President	Joe Biden
Preceded by	Eric Lander
Succeeded by	Arati Prabhakar

16th Director of the National Institutes of Health
In office
August 17, 2009 – December 19, 2021

President	Barack Obama Donald Trump Joe Biden
Deputy	Lawrence A. Tabak

Dr. Kizzmekia Corbett speaks to members of the graduating class and parents at the University of North Carolina commencement exercises Friday, May 14, 2021. BY UNC

A group of nine North Carolinians spanning the fields of microbiology and immunology, education, public service, history and fashion received the state's highest civilian honor during a ceremony Thursday evening.

Recipients of the North Carolina Award for 2021 and 2020 (since last year's ceremony was canceled due to the pandemic) include Dr. Francis Collins, the outgoing director of the National Institutes of Health who has led the federal agency for the last 12 years; Dr. Ralph Baric, a renowned coronavirus researcher at UNC-Chapel Hill; and André Leon Talley, who grew up in Durham and went on to work at several fashion publications, including Vogue.

Established by state lawmakers in 1961 and first awarded in 1964, the North Carolina Award recognizes "significant contributions to the state and nation in the fields of fine arts, literature, public service and science," according to the N.C. Department of Cultural and Natural Resources, which administers the award.

More than 250 people have received the award, including Maya Angelou, James Taylor, John Hope Franklin, the Rev. Billy Graham and the Rev. William J. Barber II.

tober 24, 2023
ition

The News&Observer

Part of the McClatchy Media Network

s Business Triangle Now Politics Sports Living Jobs/Recruiting Personal Finance Obituarie

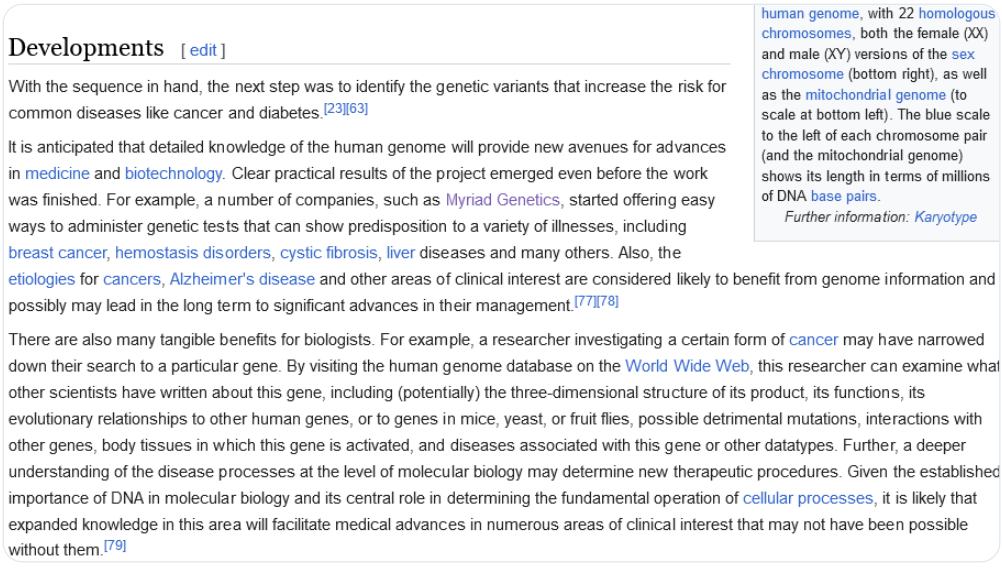
NORTH CAROLINA

Meet the 9 North Carolinians receiving the state's highest civilian honor this year

BY AVI BAJPAI

UPDATED NOVEMBER 19, 2021 10:45 AM

11🧵Here's the kicker, Collins wasn't just Fauci's boss at NIH, he also was the first director of the Human Genome Project at the Nat'l human genome Institute, of which the company leading the sequencing is none other than Myriad Genetics.



human genome, with 22 homologous chromosomes, both the female (*XX*) and male (*XY*) versions of the sex chromosome (bottom right), as well as the mitochondrial genome (to scale at bottom left). The blue scale to the left of each chromosome pair (and the mitochondrial genome) shows its length in terms of millions of DNA base pairs.

Further information: Karyotype

Developments [edit]

With the sequence in hand, the next step was to identify the genetic variants that increase the risk for common diseases like cancer and diabetes.[23][63]

It is anticipated that detailed knowledge of the human genome will provide new avenues for advances in medicine and biotechnology. Clear practical results of the project emerged even before the work was finished. For example, a number of companies, such as Myriad Genetics, started offering easy ways to administer genetic tests that can show predisposition to a variety of illnesses, including breast cancer, hemostasis disorders, cystic fibrosis, liver diseases and many others. Also, the etiologies for cancers, Alzheimer's disease and other areas of clinical interest are considered likely to benefit from genome information and possibly may lead in the long term to significant advances in their management.[77][78]

There are also many tangible benefits for biologists. For example, a researcher investigating a certain form of cancer may have narrowed down their search to a particular gene. By visiting the human genome database on the World Wide Web, this researcher can examine what other scientists have written about this gene, including (potentially) the three-dimensional structure of its product, its functions, its evolutionary relationships to other human genes, or to genes in mice, yeast, or fruit flies, possible detrimental mutations, interactions with other genes, body tissues in which this gene is activated, and diseases associated with this gene or other datatypes. Further, a deeper understanding of the disease processes at the level of molecular biology may determine new therapeutic procedures. Given the established importance of DNA in molecular biology and its central role in determining the fundamental operation of cellular processes, it is likely that expanded knowledge in this area will facilitate medical advances in numerous areas of clinical interest that may not have been possible without them.[79]

	National Institutes of Health
Thesis	*Semiclassical theory of vibrationally inelastic scattering, with application to $H^+ + H_2$* (1974)
Doctoral advisor	James Cross

Several scientific teams worked in the 1970s and 1980s to identify genes and their loci as a cause of cystic fibrosis. Progress was modest until 1985, when Lap-Chee Tsui and colleagues at Toronto's Hospital for Sick Children identified the locus for the gene.[18] It was then determined that a shortcut was needed to speed the process of identification, so Tsui contacted Collins, who agreed to collaborate with the Toronto team and share his chromosome-jumping technique. The gene was identified in June 1989,[19][20] and the results were published in the journal *Science* on September 8, 1989.[21] This identification was followed by other genetic discoveries made by Collins and a variety of collaborators. They included isolation of the genes for Huntington's disease,[22] neurofibromatosis,[23][24] multiple endocrine neoplasia type 1,[25] inv(16) AML[26] and Hutchinson–Gilford progeria syndrome.[27]

Genomics [edit]

In 1993 National Institutes of Health Director Bernadine Healy appointed Collins to succeed James D. Watson as director of the National Center for Human Genome Research, which became National Human Genome Research Institute (NHGRI) in 1997. As director he oversaw the International Human Genome Sequencing Consortium,[28] which was the group that successfully carried out the Human Genome Project.[29]

In 1994 Collins founded NHGRI's Division of Intramural Research,[30] a collection of investigator-directed laboratories that conduct genome research on the NIH campus.[*citation needed*]

In June 2000 Collins was joined by President Bill Clinton and biologist Craig Venter in making the announcement of a working draft of the human genome.[31] He stated that "It is humbling for me, and awe-inspiring to realize that we have caught the first glimpse of our own instruction book, previously known only to God."[32][33][34] An initial analysis was published in February 2001, and scientists worked toward finishing the reference version of the human genome sequence by 2003, coinciding with the 50th anniversary of James D. Watson and Francis Crick's publication of the structure of DNA.[*citation needed*]

Another major activity at NHGRI during his tenure as director was the creation of the haplotype map of the human genome. This International HapMap Project produced a catalog of human genetic variations—called single-nucleotide polymorphisms—which is now being used to discover variants correlated with disease risk. Among the labs engaged in that effort is Collins' own lab at NHGRI, which has sought to identify and understand the genetic variations that influence the risk of developing type 2 diabetes.[*citation needed*]

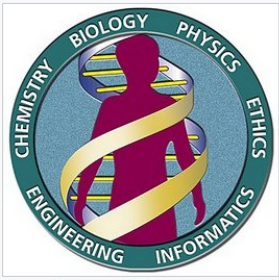
In addition to his basic genetic research and scientific leadership, Collins is known for his close attention to ethical and legal issues in genetics. He has been a strong advocate for protecting the privacy of genetic information and has served as a national leader in securing the passage of the federal Genetic Information and Nondiscrimination Act, which prohibits gene-based discrimination in employment and health insurance.[35] In 2013, spurred by concerns over the publication of the genome of the widely used HeLa cell line derived from the late Henrietta Lacks, Collins and other NIH leaders worked with the Lacks family to reach an agreement to protect their privacy, while giving researchers controlled access to the genomic data.[36]

Building on his own experiences as a physician volunteer in a rural missionary hospital in Nigeria,[37] Collins is also very interested in

Human Genome Project

From Wikipedia, the free encyclopedia

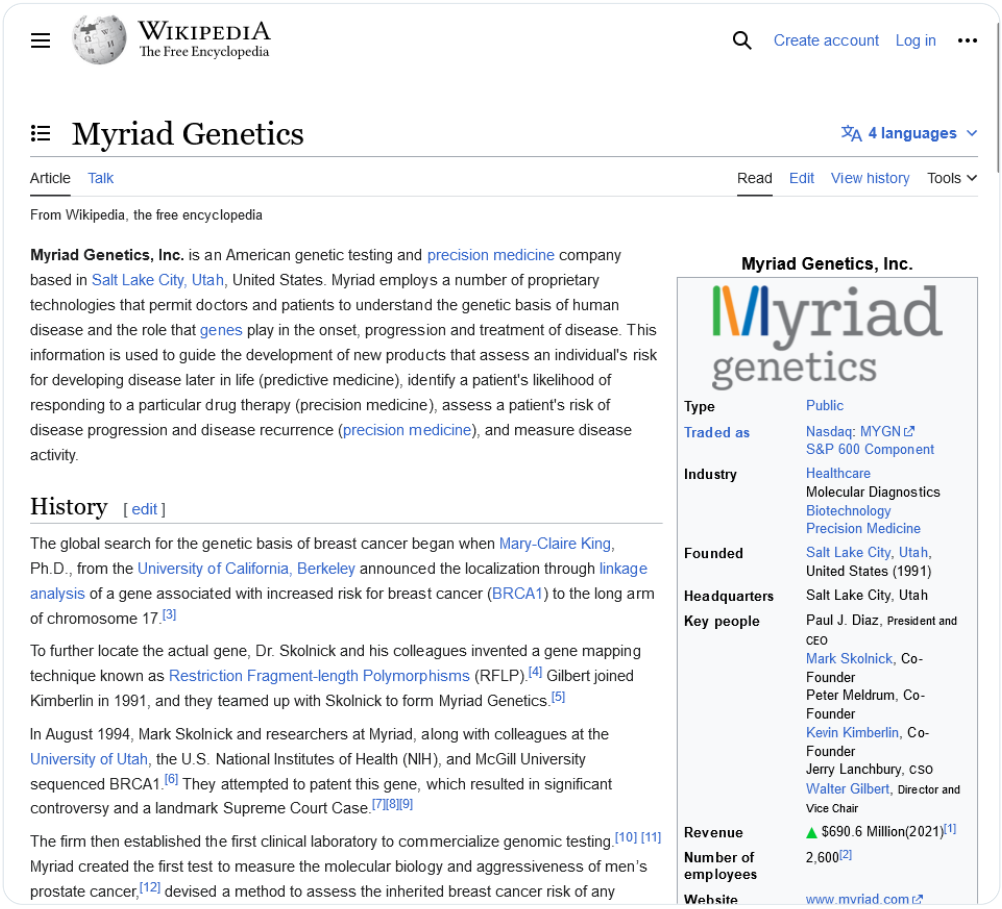
The **Human Genome Project** (**HGP**) was an international scientific research project with the goal of determining the base pairs that make up human DNA, and of identifying, mapping and sequencing all of the genes of the human genome from both a physical and a functional standpoint. It started in 1990 and was completed in 2003.[1] It remains the world's largest collaborative biological project.[2] Planning for the project started after it was adopted in 1984 by the US government, and it officially launched in 1990. It was declared complete on April 14, 2003, and included about 92% of the genome.[3] Level "complete genome" was achieved in May 2021, with a remaining only 0.3% bases covered by potential issues.[4][5] The final gapless assembly was finished in January 2022.[6]



Logo of the Human Genome Project

Funding came from the United States government through the National Institutes of Health (NIH) as well as numerous other groups from around the world. A parallel project was conducted outside the government by the Celera Corporation, or Celera Genomics, which was formally launched in 1998. Most of the government-sponsored sequencing was performed in twenty universities and research centres in the United States, the United Kingdom, Japan, France, Germany, and China,[7] working in the International Human Genome Sequencing Consortium (IHGSC).

The Human Genome Project originally aimed to map the complete set of nucleotides contained in a human haploid reference genome, of which there are more than three billion. The "genome" of any given individual is unique; mapping the "human genome" involved sequencing samples collected from a small number of individuals



Wikipedia
The Free Encyclopedia

Create account Log in

Myriad Genetics

4 languages

Article Talk | Read Edit View history Tools

From Wikipedia, the free encyclopedia

Myriad Genetics, Inc. is an American genetic testing and precision medicine company based in Salt Lake City, Utah, United States. Myriad employs a number of proprietary technologies that permit doctors and patients to understand the genetic basis of human disease and the role that genes play in the onset, progression and treatment of disease. This information is used to guide the development of new products that assess an individual's risk for developing disease later in life (predictive medicine), identify a patient's likelihood of responding to a particular drug therapy (precision medicine), assess a patient's risk of disease progression and disease recurrence (precision medicine), and measure disease activity.

History [edit]

The global search for the genetic basis of breast cancer began when Mary-Claire King, Ph.D., from the University of California, Berkeley announced the localization through linkage analysis of a gene associated with increased risk for breast cancer (BRCA1) to the long arm of chromosome 17.[3]

To further locate the actual gene, Dr. Skolnick and his colleagues invented a gene mapping technique known as Restriction Fragment-length Polymorphisms (RFLP).[4] Gilbert joined Kimberlin in 1991, and they teamed up with Skolnick to form Myriad Genetics.[5]

In August 1994, Mark Skolnick and researchers at Myriad, along with colleagues at the University of Utah, the U.S. National Institutes of Health (NIH), and McGill University sequenced BRCA1.[6] They attempted to patent this gene, which resulted in significant controversy and a landmark Supreme Court Case.[7][8][9]

The firm then established the first clinical laboratory to commercialize genomic testing.[10] [11] Myriad created the first test to measure the molecular biology and aggressiveness of men's prostate cancer,[12] devised a method to assess the inherited breast cancer risk of any

Myriad Genetics, Inc.

Myriad genetics

Type	Public
Traded as	Nasdaq: MYGN S&P 600 Component
Industry	Healthcare Molecular Diagnostics Biotechnology Precision Medicine
Founded	Salt Lake City, Utah, United States (1991)
Headquarters	Salt Lake City, Utah
Key people	Paul J. Diaz, President and CEO Mark Skolnick, Co-Founder Peter Meldrum, Co-Founder Kevin Kimberlin, Co-Founder Jerry Lanchbury, CSO Walter Gilbert, Director and Vice Chair
Revenue	▲ $690.6 Million(2021)[1]
Number of employees	2,600[2]
Website	www.myriad.com

12🧵This is a developing story worth looking into. Til then, receipts as always 🧾
https://cdn.who.int/media/docs/default-source/blue-print/2.-baric_r-d-who-consultation_march-25-2022.pdf

Scientists discover how dengue vaccine fails to protect against disease
Researchers discovered that a small subpopulation of antibodies binding to unique sites on each serotype are linked to protection. The research, published in the Journal of Clinical Investigation, pr…

https://www.eurekalert.org/news-releases/903503

archive.ph/DQreQ
https://sph.unc.edu/wp-content/uploads/sites/112/2016/09/CV_Ralph_Baric.pdf
https://www.linkedin.com/in/michelle-baric-123811a3/

Myriad Genetics - Wikipedia

https://en.wikipedia.org/wiki/Myriad_Genetics

Francis Collins - Wikipedia

https://en.wikipedia.org/wiki/Francis_Collins

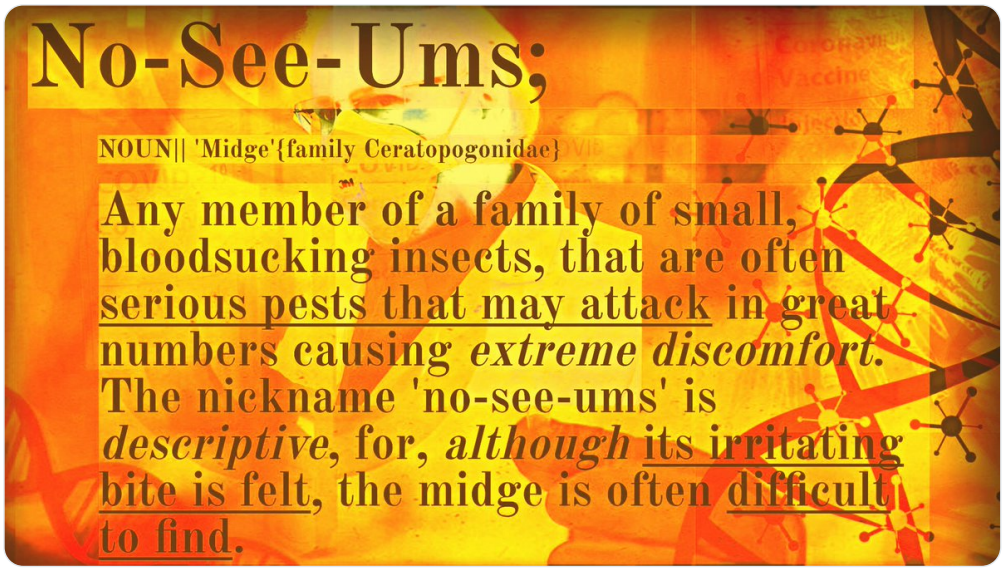
@threadreaderapp unroll

• • •

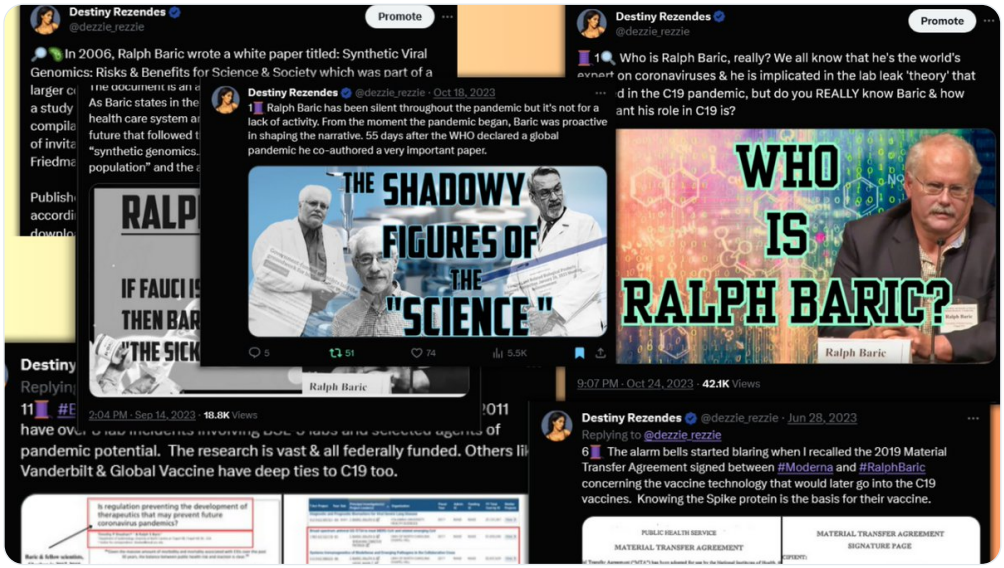
Destiny Rezendes @dezzie_rezzie

Feb 6, 2024 • 10 tweets • dezzie_rezzie/status/1754684068334092750

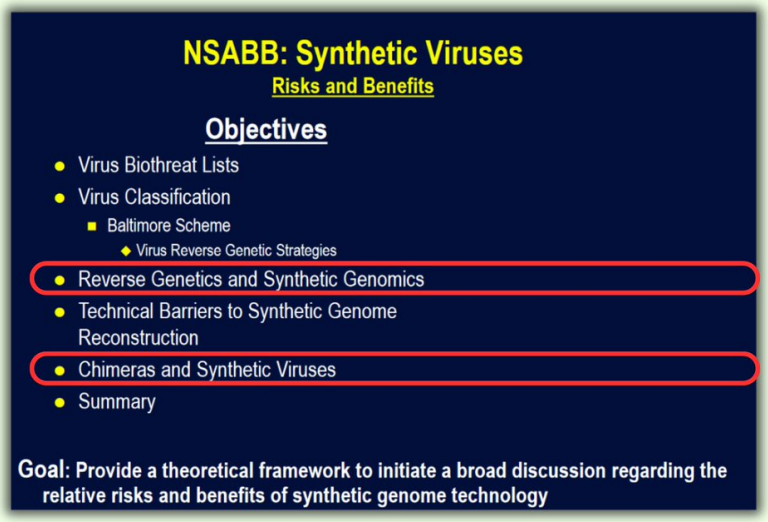
🧵1🧵Ralph Baric invented No-See-Um sites, a way to alter viruses w/o leaving a trace. The name comes from bugs local to Baric in NC. Oddly the definition of No-See-Ums describes not just the bugs, but also Baric himself. So, why did NIH allow this infestation to go unchecked?!



2🧵I've covered the Corona-Creep at length. For today's thread familiarizing yourself [if you haven't] with these threads- namely this thread about Baric's publication on Synthetic Biology 2006:



3🧵The same yr as Baric's terrifying Synthetic Genomic paper, Baric gave a presentation to the National Science Advisory Board for Biosecurity [NSABB] on Synthetic Viruses. The NSABB is the federal advisory committee that addresses threats to biosecurity and Gain of Function.



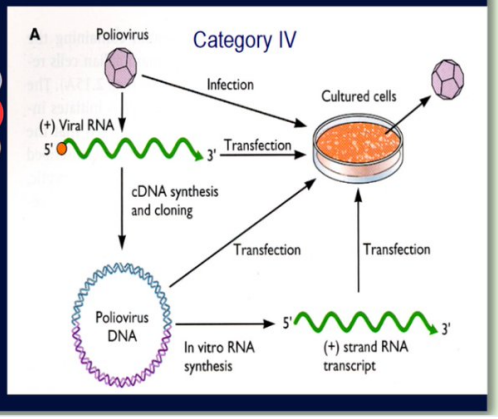
4🧵 Per Baric's NSABB presentation, Biothreat Viruses that can be created in a lab or "reverse engineered" have understood mechanisms; for instance "ALL viruses MUST transcribe genome into mRNA *for making* Viral Proteins." He lists, SARS-CoVs as easy to alter, & that the sequences to do so are "readily available."

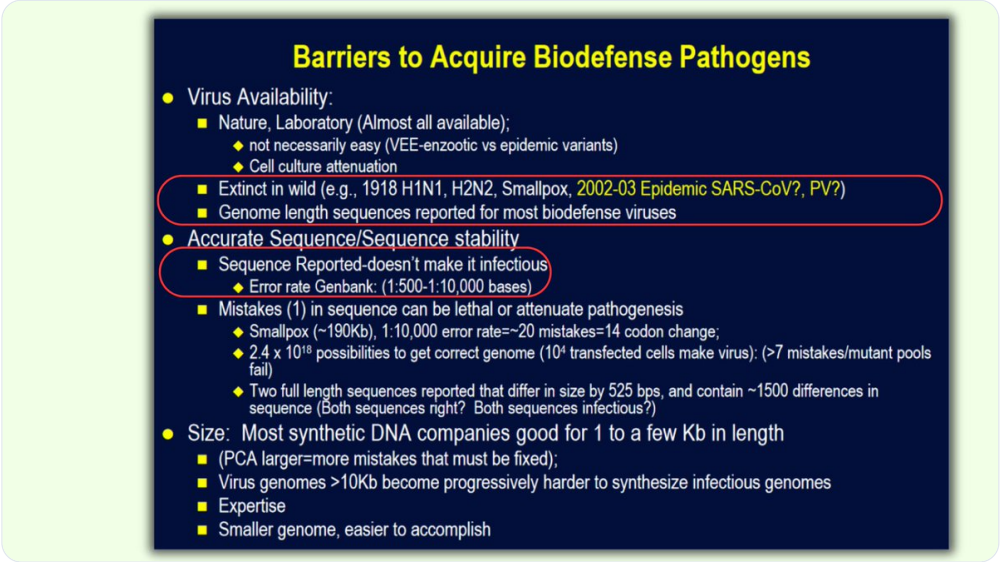
Biothreat Viruses
HHS/CDC, USDA, Dept Commerce, NIH Category A-C
(Lists of Biothreat Viruses)

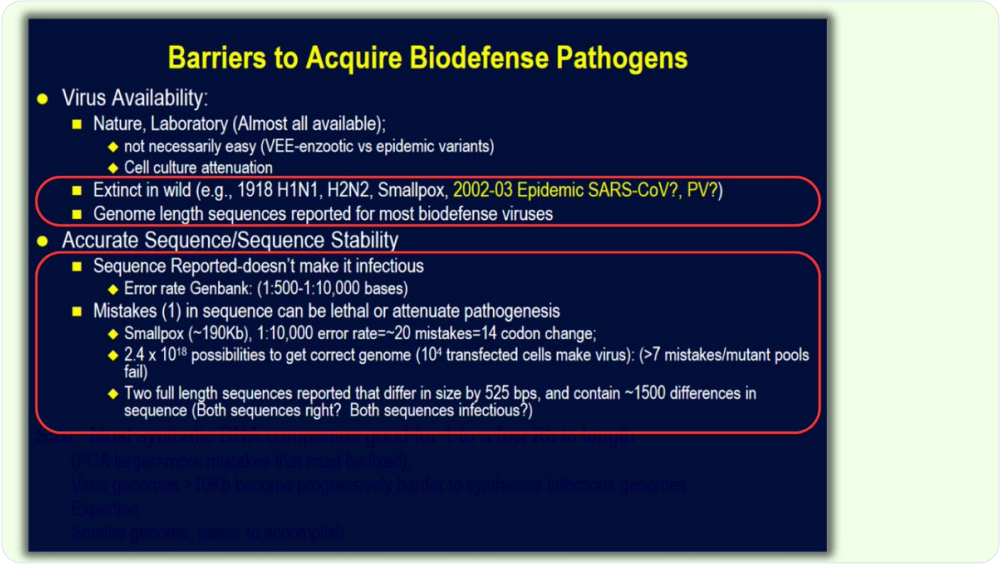
- Very Heterogeneous group of viruses
  - HHS/CDC, USDA, Dept Commerce (Lists of Biothreat Viruses)
- Different genome organizations + replication strategies
  - different approaches are needed to develop infectious genomes
  - Genomes
    - dsDNA, ssRNA (+) polarity, ssRNA (-) polarity and dsRNA
- Simple classification scheme to understand virus reverse genetic strategies
  - All viruses must transcribe genome into mRNA ⟶ viral proteins.

Virus Reverse Genetics
Category IV

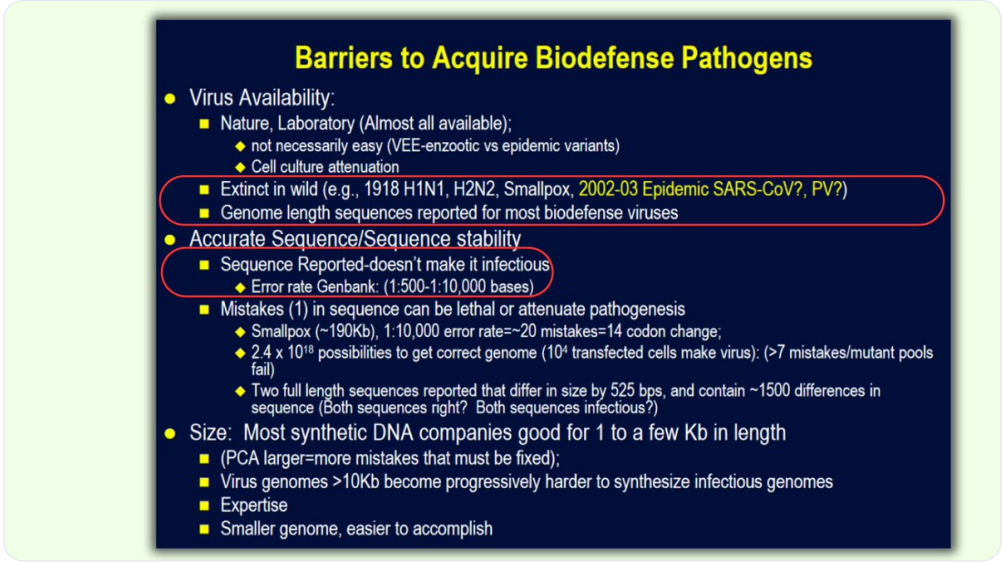
- Positive Strand RNA Viruses
  - Picornaviruses
  - Enteroviruses (e.g., PV, FMDV, HAV)
  - Coronaviruses (e.g., SARS-CoV)
  - Alphaviruses (e.g., VEE, WEE, EEE)
  - Flaviviruses (e.g., Yellow fever, dengue, etc.)
  - Noroviruses (not yet)
- Manipulate DNA and recover altered viruses
- Sequences readily available

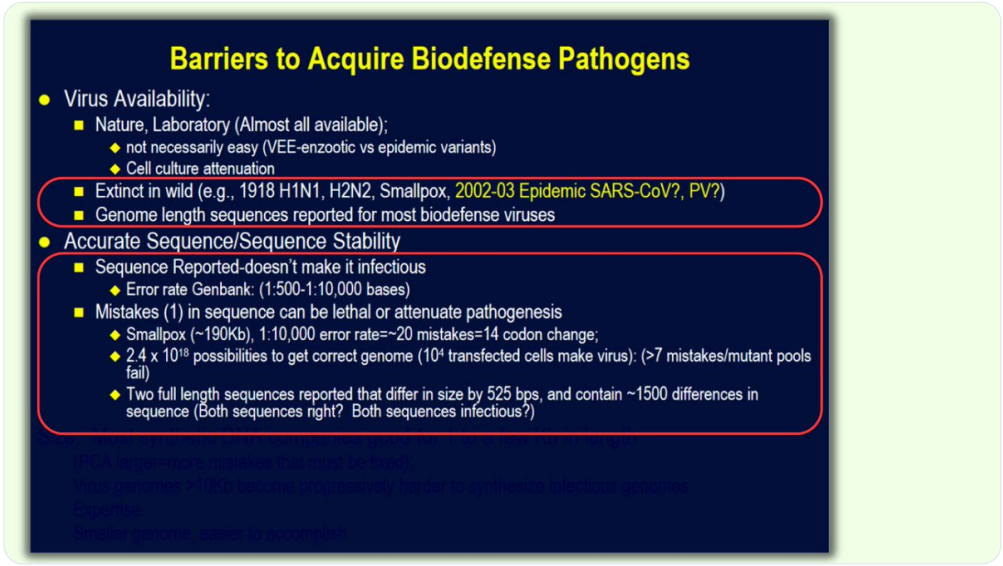






5 For barriers to biodefense Baric admits that Sequence Stability is a concern, stating that "Sequences Reported doesn't make it infectious" & that even NIH's Genbank has an alarming Error Rate of anywhere between 1:500- 1:10,000 bases! These "mistakes" can make a pathogen more lethal or attenuate parthenogenesis. 👀

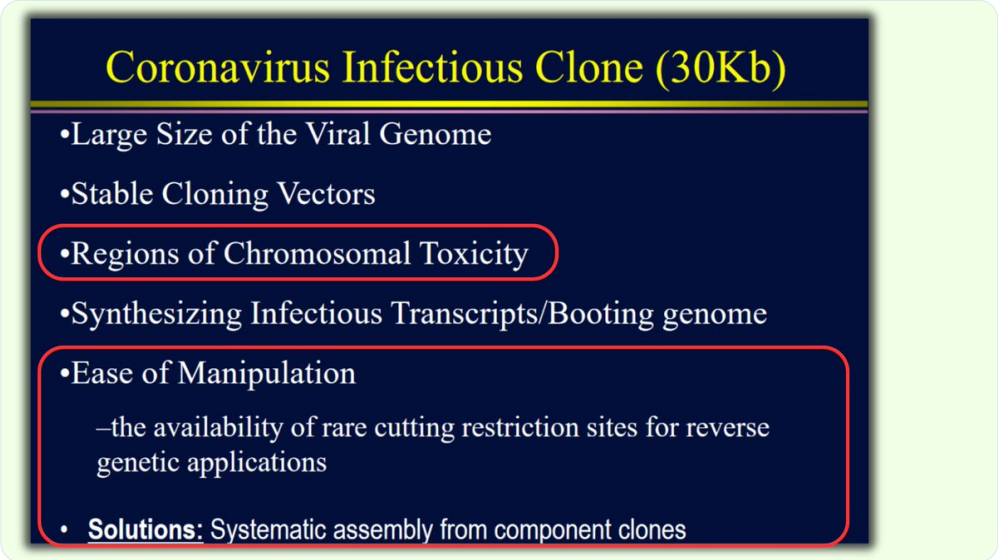




6🧵 When talking specifically about Coronavirus Infectious Clones are the easiest to manipulate but notes they have regions of "Chromosomal Toxicity."

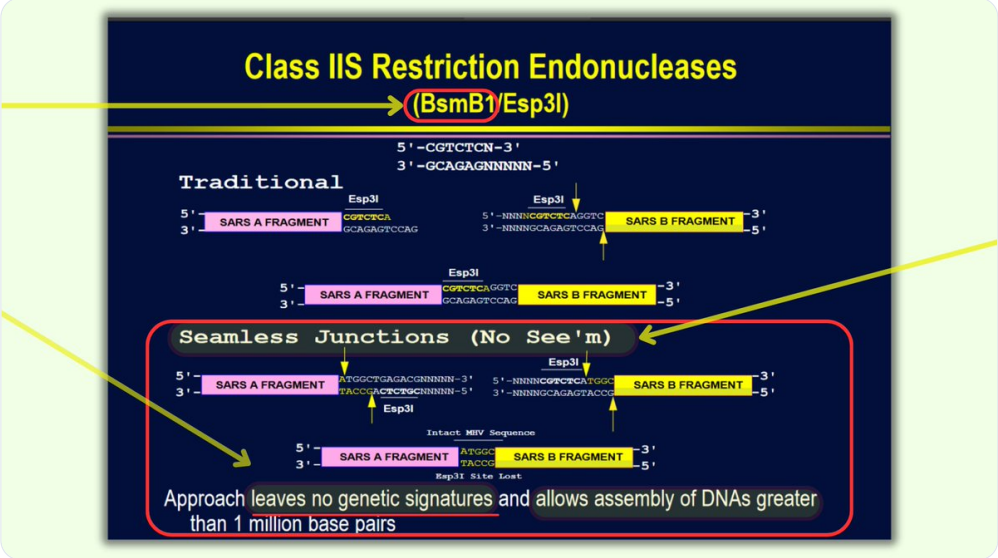
Well, what does that even mean? ⁉️

According to the NIH, Chromosomal toxicity refers to the harmful effects on the chromosomes within a cell, which can lead to DNA damage, mutations, and potentially CANCER!! ☠️



7🧵 On one slide, Baric gives the NSABB an example for how easily Coronavirus no-see-um-manipulation is done. Take note of which restriction site Endonuclease Enzymes Baric suggests: Esp31 & BsmB1.

The SAME one cited in the DARPA DEFUSE draft by EcoHealth Alliance + Ralph Baric from 2018 where they suggested its use to create pathogenic SARS-CoV chimera's. This is merely a coincidence, & even if it wasn't how could you prove it when Baric himself brags by adding to the BsmB1 slide that this "Approach leaves NO GENETIC SIGNATURES.."



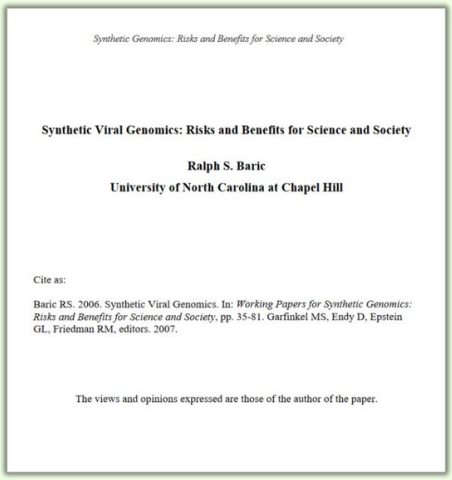
8🧵 A quick look back at that Synthetic Biology paper Baric authored in 2006 focused on Synthetic Viruses & Biological Warfare. On one page, Baric describes how a Bioterrorist would deploy these pathogens. The nonchalant way he describes these scenarios is cause for alarm all on it's own, but the actual text is a biological nightmare.

🚨👇✍️

Baric writes;

"A clever bioterrorist might start with a relatively benign, easily obtainable virus (BSL2) & obtain an existing molecular clone by simply requesting it from the scientists who work with these agents. Then, using the expanding database of genomic sequences & identified virulence genes, the benign viral genome

could be modified into more lethal combinations for nefarious use."



Synthetic Genomics: Risks and Benefits for Science and Society

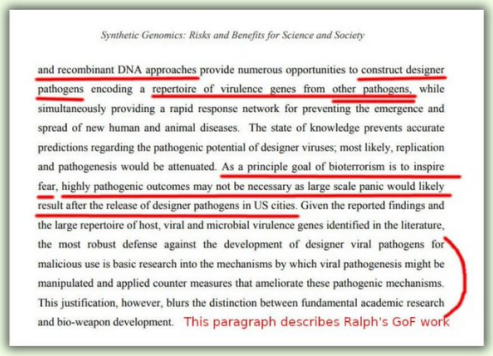
Synthetic Viral Genomics: Risks and Benefits for Science and Society

Ralph S. Baric
University of North Carolina at Chapel Hill

Cite as:

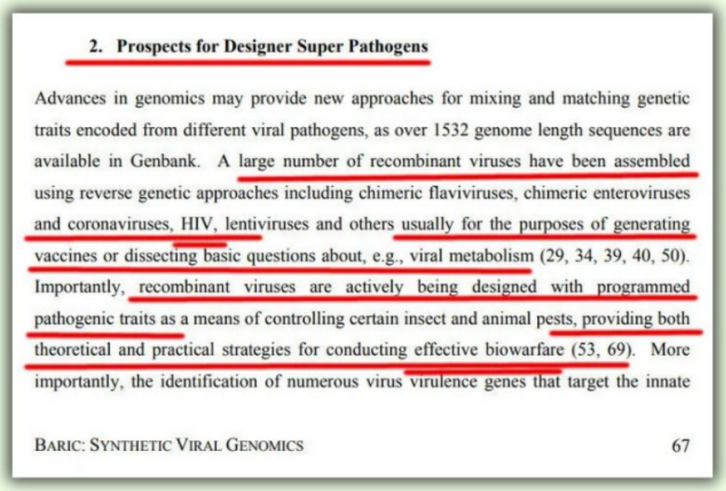
Baric RS. 2006. Synthetic Viral Genomics. In: *Working Papers for Synthetic Genomics: Risks and Benefits for Science and Society*, pp. 35-81. Garfinkel MS, Endy D, Epstein GL, Friedman RM, editors. 2007.

The views and opinions expressed are those of the author of the paper.



Synthetic Genomics: Risks and Benefits for Science and Society

and recombinant DNA approaches provide numerous opportunities to construct designer pathogens encoding a repertoire of virulence genes from other pathogens, while simultaneously providing a rapid response network for preventing the emergence and spread of new human and animal diseases. The state of knowledge prevents accurate predictions regarding the pathogenic potential of designer viruses; most likely, replication and pathogenesis would be attenuated. As a principle goal of bioterrorism is to inspire fear, highly pathogenic outcomes may not be necessary as large scale panic would likely result after the release of designer pathogens in US cities. Given the reported findings and the large repertoire of host, viral and microbial virulence genes identified in the literature, the most robust defense against the development of designer viral pathogens for malicious use is basic research into the mechanisms by which viral pathogenesis might be manipulated and applied counter measures that ameliorate these pathogenic mechanisms. This justification, however, blurs the distinction between fundamental academic research and bio-weapon development. This paragraph describes Ralph's GoF work



2. Prospects for Designer Super Pathogens

Advances in genomics may provide new approaches for mixing and matching genetic traits encoded from different viral pathogens, as over 1532 genome length sequences are available in Genbank. A large number of recombinant viruses have been assembled using reverse genetic approaches including chimeric flaviviruses, chimeric enteroviruses and coronaviruses, HIV, lentiviruses and others usually for the purposes of generating vaccines or dissecting basic questions about, e.g., viral metabolism (29, 34, 39, 40, 50). Importantly, recombinant viruses are actively being designed with programmed pathogenic traits as a means of controlling certain insect and animal pests, providing both theoretical and practical strategies for conducting effective biowarfare (53, 69). More importantly, the identification of numerous virus virulence genes that target the innate

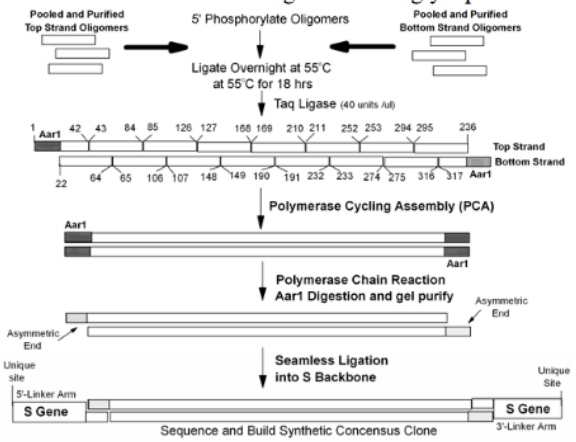
Synthetic Genomics: Risks and Benefits for Science and Society

engineering tools have been developed for only a few BW agents, making them relatively poor substrates for biodesign. A clever bioterrorist might start with a relatively benign, easily obtainable virus (BSL2) and obtain an existing molecular clone by simply requesting it from the scientists who work with these agents. Then, using the expanding database of genomic sequences and identified virulence genes, the benign viral genome could be modified into more lethal combinations for nefarious use.

Consequently, knowledgeable experts can theoretically reconstruct full length synthetic genomes for any of the high priority virus pathogens, although technical concerns may limit the robustness of these approaches. It is conceivable that a bioterrorist could order

Figure 9. PCA Technique. Synthetic Reconstruction of Exotic SARS-CoV Spike Glycoproteins.

Synthetic S glycoproteins are synthesized and inserted into the SARS-CoV molecular clone; allowing for recovery of recombinant viruses encoding zoonotic S glycoproteins.



9 Baric also writes what he thinks a BioTerror attack using a lab created virus would look like. You tell me if his description sounds familiar... "the release & subsequent discovery of a synthetically derived virus bioweapon will certainly garner tremendous media coverage, inspire fear & terrorize human populations."

Will synthetic or recombinant bioweapons be developed for BW use? If the main purpose is to kill and inspire fear in human populations, natural source pathogens likely provide a more reliable source of starting material. Stealing the BW agent from a laboratory or obtaining the pathogen from natural outbreak conditions is still easier than the synthetic reconstruction of a pathogenic virus. These conditions, however, change as 1st and 2nd generation candidate vaccines and drugs are developed against this select list of pathogens, limiting future attempts to newly emerged viruses. If notoriety, fear and directing foreign government policies are principle objectives, then the release and subsequent discovery of a synthetically derived virus bioweapon will certainly garner tremendous media coverage, inspire fear and terrorize human populations and direct severe pressure on government officials to respond in predicted ways.

10 Lastly, remember what Baric said about the benefits of his synthetic No-See-Um method compared to prior/classic techniques;

"Recombinant viruses generated from classic recombinant DNA techniques will carry the signature of the parental virus used in the process as well as novel restriction sites that were engineered into the genome during the cloning process.

In contrast, synthetic viral genomes can be designed to be identical with exact virus strains circulating in any given location from any year. This powerful technique provides the bioterrorist with a “scapegoat” option; leaving a sequence signature that misdirects efforts at tracking the true originators of the crime."

The only question you should have is since this is true and well documented then WHY has congress NOT called Ralph Baric in to publicly testify or at least be thoroughly investigated.
It's a tough and ugly question that likely won't be resolved and that's because the answer may very well be much, much, MUCH worse. 🔍

during the cloning process. In contrast, synthetic viral genomes can be designed to be

identical with exact virus strains circulating in any given location from any year. This powerful technique provides the bioterrorist with a "scapegoat" option; leaving a sequence signature that misdirects efforts at tracking the true originators of the crime. Even better, the approach could be used to build mistrust and/or precipitate open warfare between nations. A simple example might involve the use of the picornavirus foot and mouth disease virus, which is not present on the North American continent, yet is

1st and 2nd generation candidate vaccines and drugs are developed against this select list of pathogens, limiting future attempts to newly emerged viruses. If notoriety, fear and directing foreign government policies are principle objectives, then the release and subsequent discovery of a synthetically derived virus bioweapon will certainly garner tremendous media coverage, inspire fear and terrorize human populations and direct severe pressure on government officials to respond in predicted ways.

2. Prospects for Designer Super Pathogens

Advances in genomics may provide new approaches for mixing and matching genetic traits encoded from different viral pathogens, as over 1532 genome length sequences are available in Genbank. A large number of recombinant viruses have been assembled using reverse genetic approaches including chimeric flaviviruses, chimeric enteroviruses and coronaviruses, HIV, lentiviruses and others usually for the purposes of generating vaccines or dissecting basic questions about, e.g., viral metabolism (29, 34, 39, 40, 50). Importantly, recombinant viruses are actively being designed with programmed pathogenic traits as a means of controlling certain insect and animal pests, providing both theoretical and practical strategies for conducting effective biowarfare (53, 69). More importantly, the identification of numerous virus virulence genes that target the innate

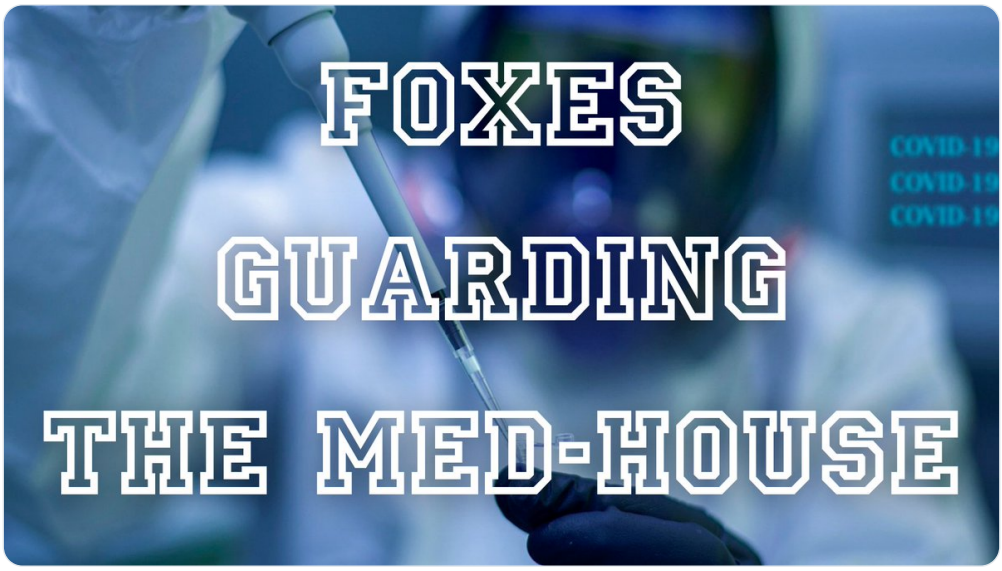

GS-5734
R.Baric
RESOURCES:
https://osp.od.nih.gov/wp-content/uploads/Baric-Synthetic_Viruses_Risks_and_Benefits.pdf
https://dspace.mit.edu/bitstream/handle/1721.1/39652/Baric%20Synthetic%20Viral%20Genomics.pdf
https://comedonchisciotte.org/la-descrizione-di-ralph-baric-dellarma-biologica-perfetta-sembra-terribilmente-simile-al-sars-cov-2/
MRNA-1273

• • •

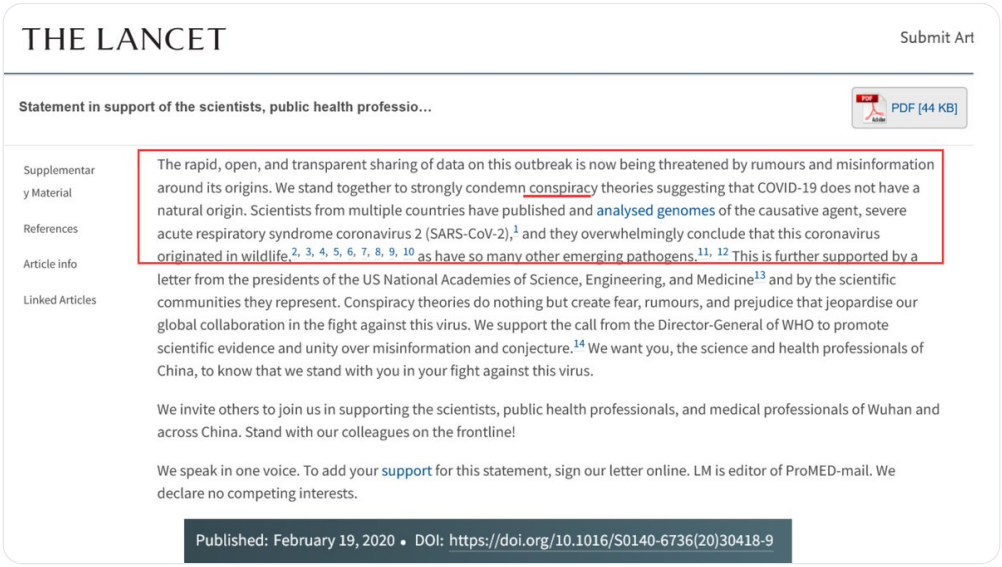
Destiny Rezendes @dezzie_rezzie

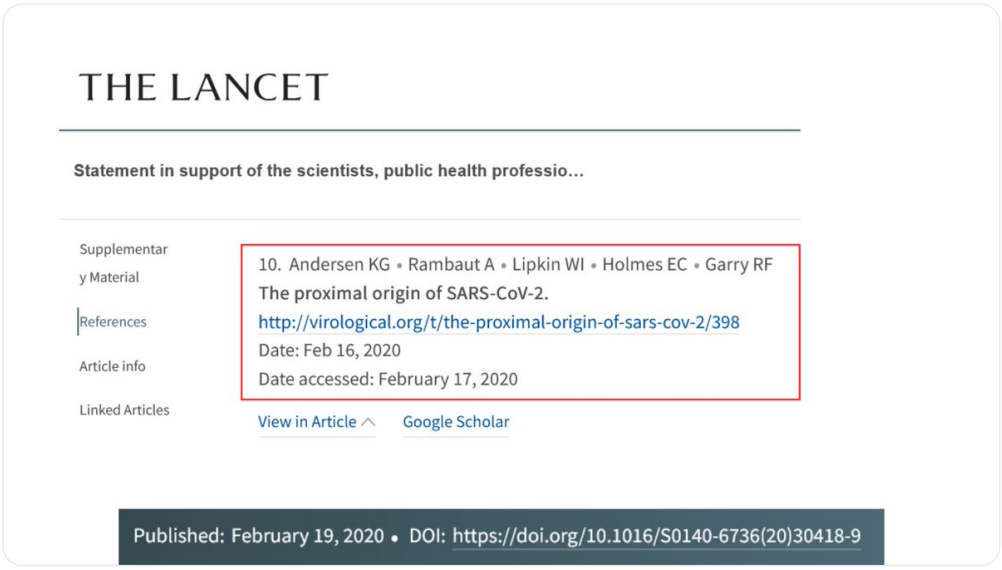
Dec 2, 2023 • 13 tweets • dezzie_rezzie/status/1731093081661772169

1🧵Continuing w/ my recent threads exposing the Conflicts of Interest [COI] in the oversight efforts & early investigations of the pandemic. I have more data to prove to you that this 'Scamdemic' is a certified rigged racket.



2🧵40 days after the C19 genome was made public a group of "concerned" scientists submitted a statement to stand in support of "the science" in Wuhan. Admonishing the "conspiracy theories" floating around of a lab leak. Published in the lancet, it is a certified fraud.





3🧵The paper was signed by a slew of implicated characters; Dennis Carroll [ex USAID] & he is joined by fellow EHA heads Karesh, Mazet, Field, & Daszak. NIH cronies like Palese, Turner & Perlman. The Wellcome Trust poster child Jeremy Farrar & virologist Linda Saif 🤫

of 2019 novel coronavirus disease (COVID-19) and are deeply concerned about its impact on global health and wellbeing. We have watched as the scientists, public health professionals, and medical professionals of China, in particular, have worked diligently and effectively to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. This effort has been remarkable.

We sign this statement in solidarity with all scientists and health professionals in China who continue to save lives and protect global health during the challenge of the COVID-19 outbreak. We are all in this together, with our Chinese counterparts in the forefront, against this new viral threat.

The rapid, open, and transparent

We invite others to join us in supporting the scientists, public health professionals, and medical professionals of Wuhan and across China. Stand with our colleagues on the frontline!

We speak in one voice. To add your support for this statement, sign our letter online. LM is editor of ProMED-mail. We declare no competing interests.

Charles Calisher, Dennis Carroll, Rita Colwell, Ronald B Corley, Peter Daszak, Christian Drosten, Luis Enjuanes, Jeremy Farrar, Hume Field, Josie Golding, Alexander Gorbalenya, Bart Haagmans, James M Hughes, William B Karesh, Gerald T Keusch, Sai Kit Lam, Juan Lubroth, John S Mackenzie, Larry Madoff, Jonna Mazet, Peter Palese, Stanley Perlman, Leo Poon, Bernard Roizman, Linda Saif, Kanta Subbarao, Mike Turner

COVID19statement@gmail.com

The rapid, open, and transparent sharing of data on this outbreak is now being threatened by rumours and misinformation around its origins. We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin. Scientists from multiple countries have published and analysed genomes of the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2),[1] and they overwhelmingly conclude that this coronavirus originated in wildlife,[2-10] as have so many other emerging pathogens.[11,12] This is further supported by a letter from the presidents of the US National Academies of Science, Engineering, and Medicine[13] and by the scientific communities they represent. Conspiracy theories do

Correspondence

Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19

We are public health scientists who have closely followed the emergence of 2019 novel coronavirus disease (COVID-19) and are deeply concerned about its impact on global health and wellbeing. We have watched as the scientists, public health professionals, and medical professionals of China, in particular, have worked diligently and effectively to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. This effort has been remarkable.

We sign this statement in solidarity with all scientists and health professionals in China who continue to save lives and protect global health during the challenge of the COVID-19 outbreak. We are all in this together, with our Chinese counterparts in the forefront, against this new viral threat.

The rapid, open, and transparent sharing of data on this outbreak is now being threatened by rumours and misinformation around its origins. We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin. Scientists from multiple countries have published and analysed genomes of the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2),[1] and they overwhelmingly conclude that this coronavirus originated in wildlife,[2–10] as have so many other emerging pathogens.[11,12] This is further supported by a letter from the presidents of the US National Academies of Science, Engineering, and Medicine[13] and by the scientific communities they represent. Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus. We support the call from the Director-General of WHO to promote scientific evidence and unity over misinformation and conjecture.[14] We want you, the science and health professionals of China, to know that we stand with you in your fight against this virus.

We invite others to join us in supporting the scientists, public health professionals, and medical professionals of Wuhan and across China. Stand with our colleagues on the frontline!

We speak in one voice. To add your support for this statement, sign our letter online. I M is editor of ProMED-mail. We declare no competing interests.

Charles Calisher, Dennis Carroll, Rita Colwell, Ronald B Corley, Peter Daszak, Christian Drosten, Luis Enjuanes, Jeremy Farrar, Hume Field, Josie Golding, Alexander Gorbalenya, Bart Haagmans, James M Hughes, William B Karesh, Gerald T Keusch, Sai Kit Lam, Juan Lubroth, John S Mackenzie, Larry Madoff, Jonna Mazet, Peter Palese, Stanley Perlman, Leo Poon, Bernard Roizman, Linda Saif, Kanta Subbarao, Mike Turner

COVID19statement@gmail.com

Colorado State University, Fort Collins, CO, USA (CC); Scowcroft Institute of International Affairs, Texas A&M, College Station, TX, USA (DC); University of Maryland, College Park, MD, USA (RC); NEIDL Institute (RBC), Boston University (GTIC), Boston, MA, USA; EcoHealth Alliance, New York, NY, USA (PD); Charité – Universitatsmedizin Berlin, Berlin, Germany (CD); National Center of Biotechnology, Madrid, Spain (LE); The Wellcome Trust, London, UK (JF, JG, MT); School of Veterinary Science, The University of Queensland, Brisbane, QLD, Australia (HF); Leiden University Medical Center, Leiden, Netherlands (AG); Erasmus Medical Center, Rotterdam, Netherlands (BH); Emory University, Atlanta, GA, USA (JMH); World Organization for Animal Health (OIE) Working Group on Wildlife, New York, NY, USA (WIBG); University of Malaya, Kuala Lumpur, Malaysia (SKL); Food and Agriculture Organization of the United Nations, Rome, Italy (JL); Curtin University, Perth, WA, Australia (JSMi); Massachusetts Medical School, Worcester, MA, USA (LM); University of California at Davis, Davis, CA, USA (JM); Department of Microbiology, Icahn School of Medicine, Mt Sinai Hospital, New York, NY, USA (PP); University of Iowa, Roy J and Lucille A Carver College of Medicine, Iowa City, IA, USA (SP); The University of Hong Kong, Hong Kong (LP), University of Chicago, Chigaco, IL, USA (BR); The Ohio State University, Columbus, OH, USA (LS); and The University of Melbourne, Melbourne, VIC, Australia (KS)

1 Gorbalenya AE, Baker SC, Baric RS, et al. Severe acute respiratory syndrome-related coronavirus: the species and its viruses—a statement of the Coronavirus Study Group. *bioRxiv* 2020; published online Feb 11. DOI:2020.02.07.937862 (preprint).

2 Zhou P, Yang X-L, Wang X-G, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020; published online Feb 3. DOI:10.1038/s41586-020-2012-7.

3 Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020; published online Jan 30. https://doi.org/10.1016/S0140-6736(20)30251-8.

4 Zhu N, Zhang D, Wang W, et al. A novel coronavirus from patients with pneumonia in China, 2019. *NEJM* 2020; published online Jan 24. DOI:10.1056/NEJMoa2001017.

5 Ren L, Wang Y-M, Wu Z-Q, et al. Identification of a novel coronavirus causing severe pneumonia in humans: a descriptive study. *Chin Med J* 2020; published online Feb 11. DOI:10.1097/CM9.0000000000000722.

6 Paraskevis D, Kostaki EG, Magiorkinis G, Panayiotakopoulos G, Tsiodras S. Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event. *Infect Genet Evol* 2020; published online Jan 29. DOI:10.1016/j.meegid.2020.104212.

7 Benvenuto D, Giovanetti M, Ciccozzi A, Spoto S, Angeletti S, Ciccozzi M. The 2019-new coronavirus epidemic: evidence for virus evolution. *J Med Virol* 2020; published online Jan 29. DOI:10.1002/jmv.25688.

8 Wan Y, Shang J, Graham R, Baric RS, Li F. Receptor recognition by novel coronavirus from Wuhan: an analysis based on decade-long structural studies of SARS. *J Virol* 2020; published online Jan 29. DOI:10.1128/JVI.00127-20.

9 US Center for Disease Control and Prevention. Coronavirus disease 2019 (COVID-19) situation summary. Feb 16, 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html (accessed Feb 8, 2020).

10 Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. Feb 16, 2020. http://virological.org/t/the-proximal-origin-of-sars-cov-2/398 (accessed Feb 17, 2020).

11 Bengis R, Leighton F, Fischer J, Artois M, Morner T, Tate C. The role of wildlife in emerging and re-emerging zoonoses. *Rev Sci Tech* 2004; 23: 497–511.

12 Woolhouse ME, Gowtage-Sequeria S. Host range and emerging and reemerging pathogens. *Emerg Infect Dis* 2005; 11: 1842–47.

13 NASEM. The National Academies of Science Engineering and Medicine of the USA. NAS, NAE, and NAM presidents' letter to the White House Office of Science and Technology Policy. Feb 6, 2020. https://www.nationalacademies.org/includes/NASEMs%20Responses%20to%20OSTPs%20re%20Coronavirus_February%206,%202020.pdf (accessed Feb 7, 2020).

Published Online February 18, 2020 https://doi.org/10.1016/S0140-6736(20)30418-9

For the Chinese translation see Online for appendix

To register your support see http://chng.it/5DpTBy8T

For the SARS-CoV-2 genome analysis see https://www.gisaid.org/epiflu-applications/next-betacov-app/

Submissions should be made via our electronic submission system at http://ees.elsevier.com/thelancet/

4🧵The paper uses the CIA-Warren Commission Era tactic of tossing around the label of "conspiracy theorist" to ostracize those against the corrupt narrative. Ralph Baric is the first reference they cited & the Proximal Origins paper & WE are the conspiracy theorists?! 👀

Hong Kong, Hong Kong (LP); University of Chicago, Chigaco, IL, USA (BR); The Ohio State University, Columbus, OH, USA (LS); and The University of Melbourne, Melboune, VIC, Australia (KS)

1 Gorbalenya AE, Baker SC, Baric RS, et al. Severe acute respiratory syndrome-related coronavirus: the species and its viruses—a statement of the Coronavirus Study Group. *bioRxiv* 2020; published online Feb 11. DOI:2020.02.07.937862 (preprint).

Published Online February 18, 2020 https://doi.org/10.1016/S0140-6736(20)30418-9

For the Chinese translation see Online for appendix

9 US Center for Disease Control and Prevention. Coronavirus disease 2019 (COVID-19) situation summary. Feb 16, 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html (accessed Feb 8, 2020).

10 Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. Feb 16, 2020; http://virological.org/t/the-proximal-origin-of-sars-cov-2/398 (accessed Feb 17, 2020).

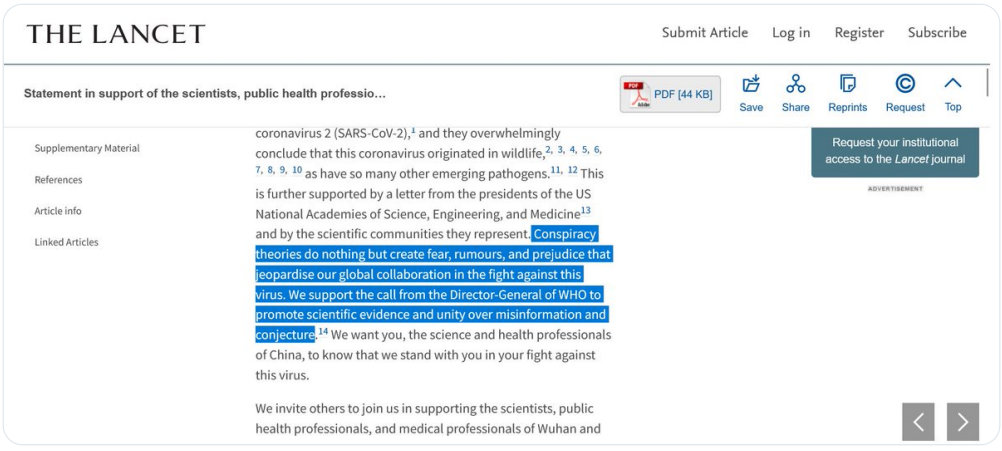
11 Bengis R, Leighton F, Fischer J, Artois M, Morner T, Tate C. The role of wildlife in emerging and re-emerging zoonoses. *Rev Sci Tech* 2004; **23:** 497–512.

12 Woolhouse ME, Gowtage-Sequeria S. Host range and emerging and reemerging pathogens. *Emerg Infect Dis* 2005; **11:** 1842–47.

13 NASEM. The National Academies of Science Engineering and Medicine of the USA. NAS, NAE, and NAM presidents' letter to the White House Office of Science and Technology Policy. Feb 6, 2020. https://www.nationalacademies.org/includes/NASEM%20Response%20to%20OSTP%20re%20Coronavirus_February%206,%202020.pdf (accessed Feb 7, 2020).

For the **SARS-CoV-2 genome analysis** see https://www.gisaid.org/epiflu-applications/next-betacov-app/

Submissions should be made via our electronic submission system at http://ees.elsevier.com/thelancet/



5🧵To me, Linda Saif is the red flag in the authors listed. A NAS Ohio State virologist who assisted the WHO during the 2003 SARS outbreak was a familiar name from FOIA'd emails between Baric, Daszak & Fauci from early on in 2020.

February 12, 2020

From: Su, Lishan <lishan_su@med.unc.edu>
Sent: Wednesday, February 12, 2020 1:12 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: A commentary on 2019 nCoV vs lab engineered viruses

Hi Ralph:

In response to the EMI journal editor's request, Drs. Shan-Lu Liu, Lin Saif and myself are writing a commentary (1-2 pages) to dispute the rumors of 2019 nCoV origin. Will you be interested, and have time, to have a quick read/comment? Please let me know if you have time.

Tentative Title: Is 2019-nCoV laboratory origin?

Thanks!

-Lishan

February 12, 2020

From: Saif, Linda
To: Liu, Shan-Lu; lishan_su@med.unc.edu
Subject: FW: A commentary on 2019 nCoV vs lab engineered viruses
Date: Wednesday, February 12, 2020 1:28:39 PM
Attachments: EMI-2019-nCoV_Commentary LJS_SLL_Refs-rsb.docx

Hi
Please note that Ralph made these changes on an earlier copy sent to him so hopefully the 2 of you can incorporate them into the updated draft I sent this AM!
Regards,
Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

February 12, 2020

From: Su, Lishan <lishan_su@med.unc.edu>
Sent: Wednesday, February 12, 2020 10:11 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: A commentary on 2019 nCoV vs lab engineered viruses

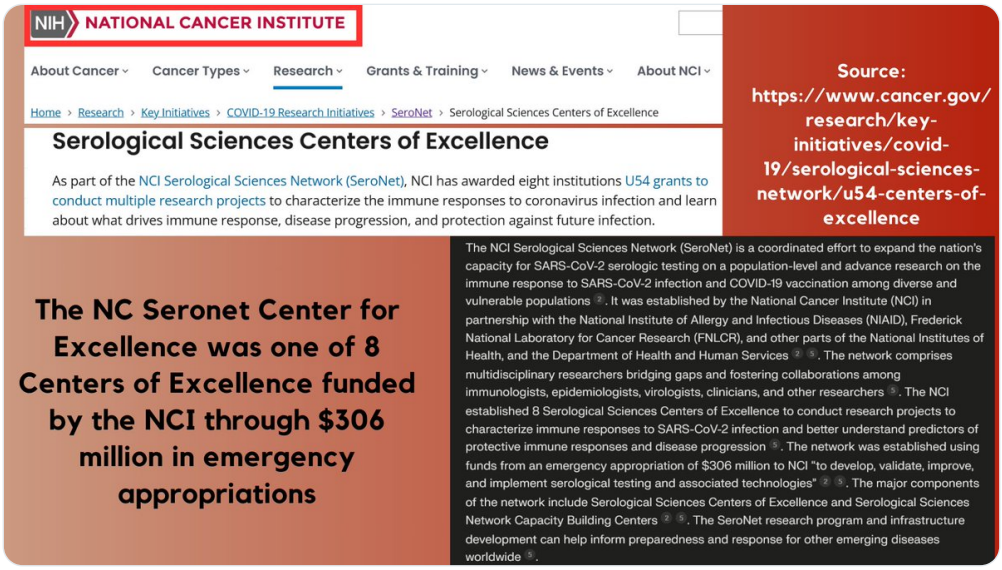
Hi Ralph:
We are trying to finish it and had no plan to get you too involved, but I do value your input. It is almost final and we are also getting comments from Perlman and Weiss.
Thanks,

-Lishan

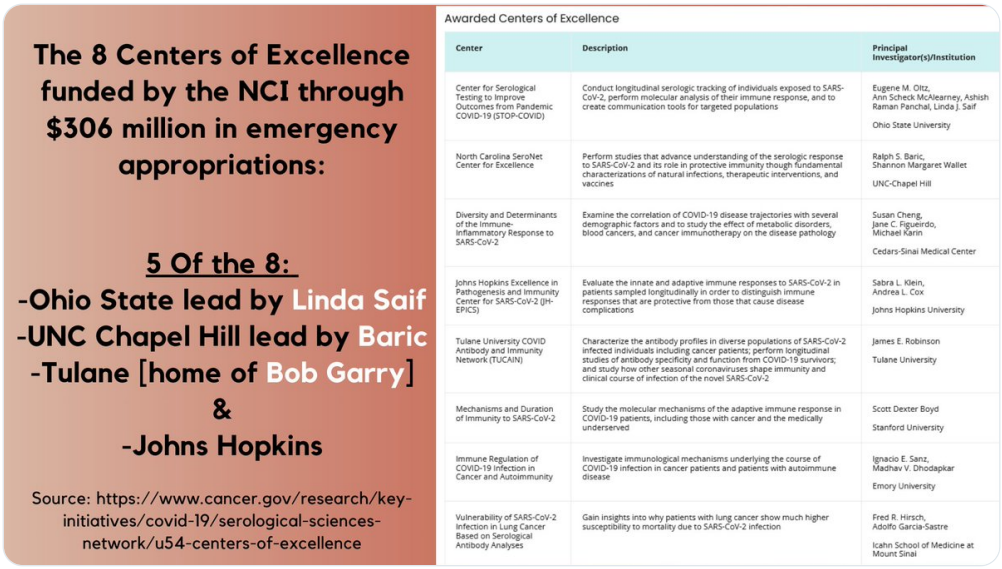
From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Wednesday, February 12, 2020 at 10:02 AM
To: "Su, Lishan" <lishan_su@med.unc.edu>
Subject: RE: A commentary on 2019 nCoV vs lab engineered viruses

sure, but don't want to be cited in as having commented prior to submission.

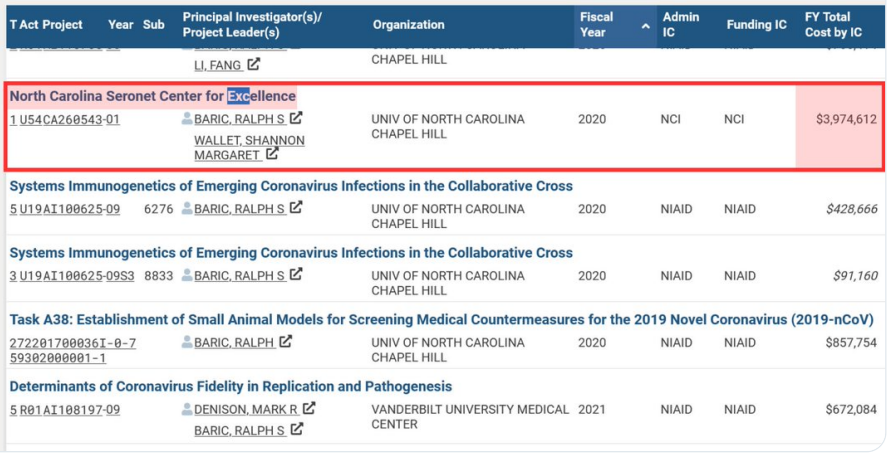
6🧵The emails show Saif and her co-workers emailing Baric about the paper in support of the Wuhan research. Why was she so concerned? I think I know why. While researching Baric's grants I found one for the NC Seronet Center for Excellence [NCSCE] Turns out the NCSCE is new!



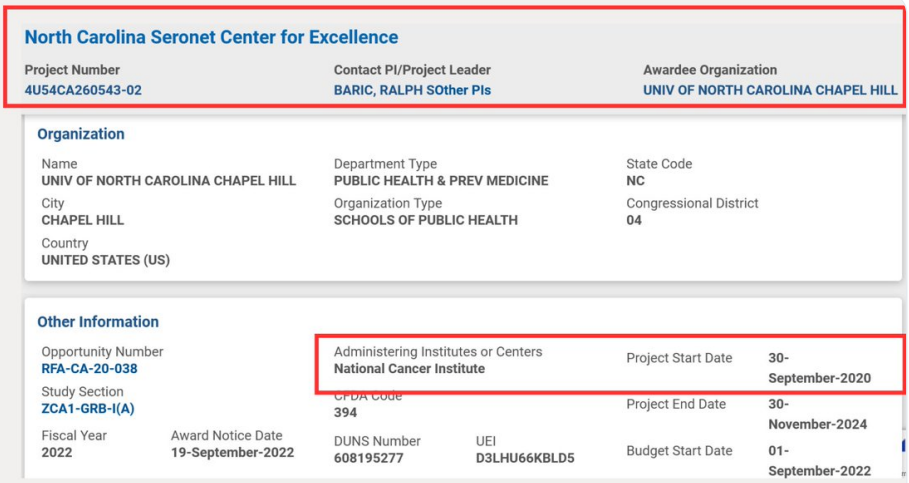
7🧵The NCSCE is one of 8 "Centers of Excellence" established w/a $306M fund- not by NIAID, but rather the National Cancer Institute even though the focus is on C19.🤔 Of the lucky 8 Centers created, Linda Saif of Ohio State was a recipient of a center just like Baric.💰😳



Also in 2020, Baric receives a grant through the North Carolina Seronet Center for Excellence but its not funded by NIH/NIAID but rather by the National Cancer Institute for $3.9 Million dollars



T Act Project	Year	Sub	Principal Investigator(s)/ Project Leader(s)	Organization	Fiscal Year	Admin IC	Funding IC	FY Total Cost by IC
			LI, FANG	CHAPEL HILL				
North Carolina Seronet Center for Excellence								
1 U54CA260543-01			BARIC, RALPH S WALLET, SHANNON MARGARET	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NCI	NCI	$3,974,612
Systems Immunogenetics of Emerging Coronavirus Infections in the Collaborative Cross								
5 U19AI100625-09		6276	BARIC, RALPH S	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NIAID	NIAID	*$428,666*
Systems Immunogenetics of Emerging Coronavirus Infections in the Collaborative Cross								
3 U19AI100625-09S3		8833	BARIC, RALPH S	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NIAID	NIAID	*$91,160*
Task A38: Establishment of Small Animal Models for Screening Medical Countermeasures for the 2019 Novel Coronavirus (2019-nCoV)								
272201700036I-0-7 59302000001-1			BARIC, RALPH	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NIAID	NIAID	$857,754
Determinants of Coronavirus Fidelity in Replication and Pathogenesis								
5 R01AI108197-09			DENISON, MARK R BARIC, RALPH S	VANDERBILT UNIVERSITY MEDICAL CENTER	2021	NIAID	NIAID	$672,084



North Carolina Seronet Center for Excellence

Project Number	Contact PI/Project Leader	Awardee Organization
4U54CA260543-02	BARIC, RALPH SOther PIs	UNIV OF NORTH CAROLINA CHAPEL HILL

Organization

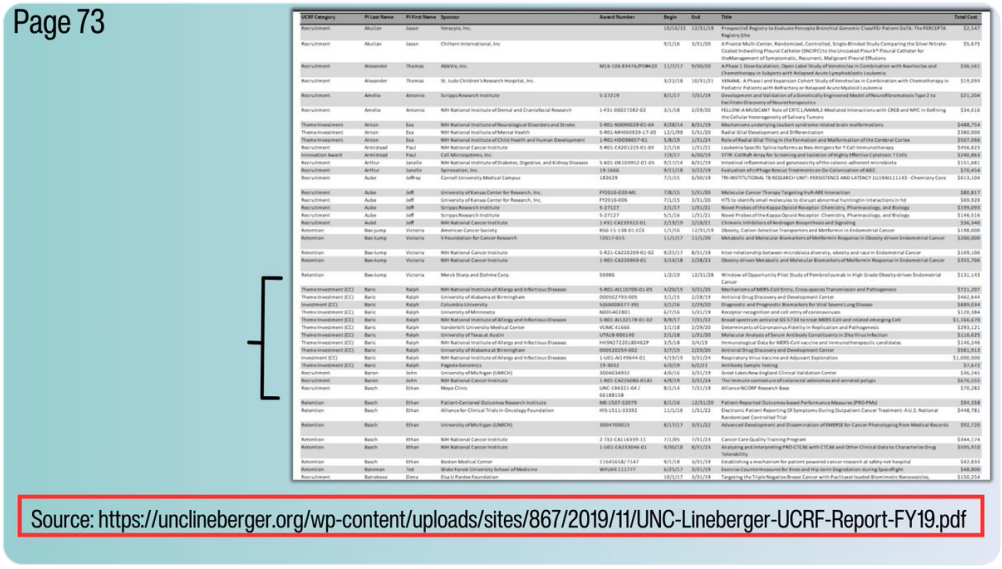
Name UNIV OF NORTH CAROLINA CHAPEL HILL	Department Type PUBLIC HEALTH & PREV MEDICINE	State Code NC
City CHAPEL HILL	Organization Type SCHOOLS OF PUBLIC HEALTH	Congressional District 04
Country UNITED STATES (US)		

Other Information

Opportunity Number RFA-CA-20-038		Administering Institutes or Centers National Cancer Institute	Project Start Date	30-September-2020
Study Section ZCA1-GRB-I(A)		CFDA Code 394	Project End Date	30-November-2024
Fiscal Year 2022	Award Notice Date 19-September-2022	DUNS Number 608195277	UEI D3LHU66KBLD5	Budget Start Date 01-September-2022

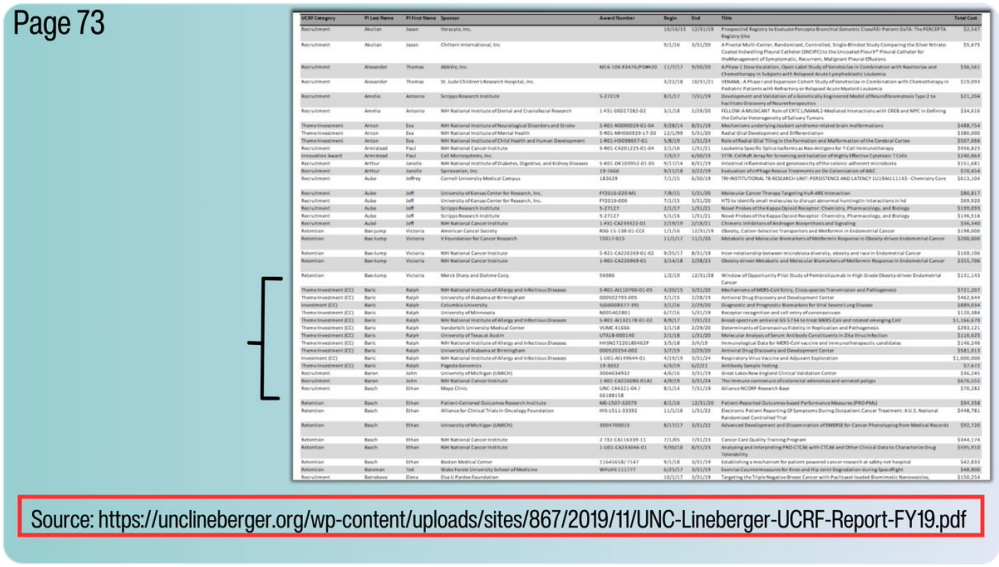
8🧵Are you surprised by the funding being from NCI? I wasn't & only because I found that since 2019 more & more funds are going to Baric and not through NIH as much, but through the NCI. I have proof of this in UNC's Lineberger Cancer Institute's funding report for 2019...

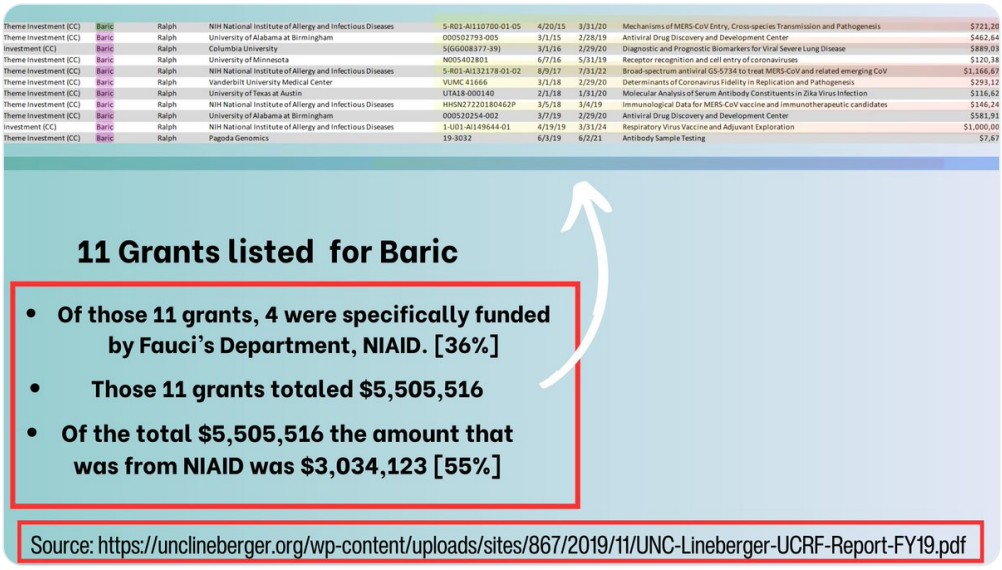
Source: https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf



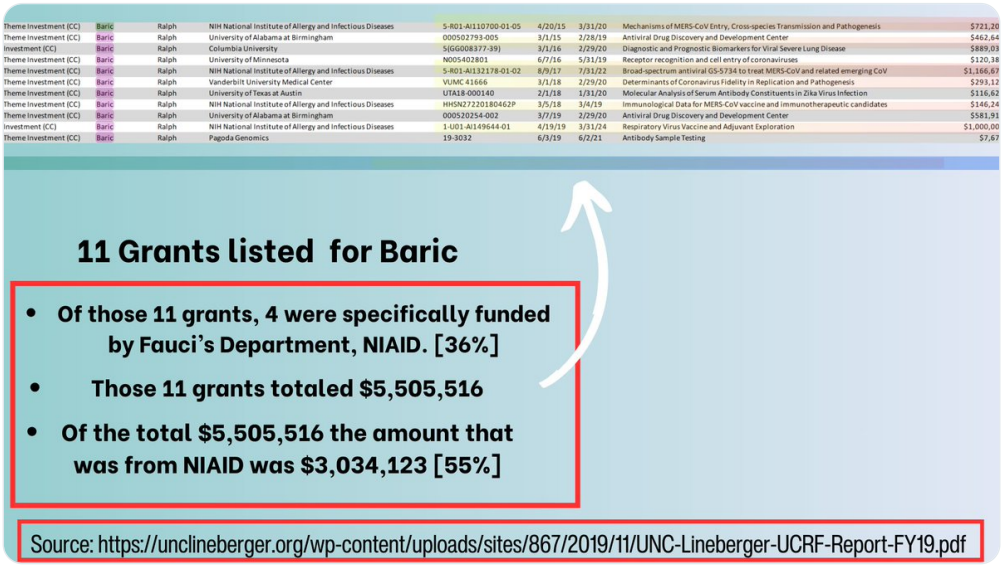
Source: https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf

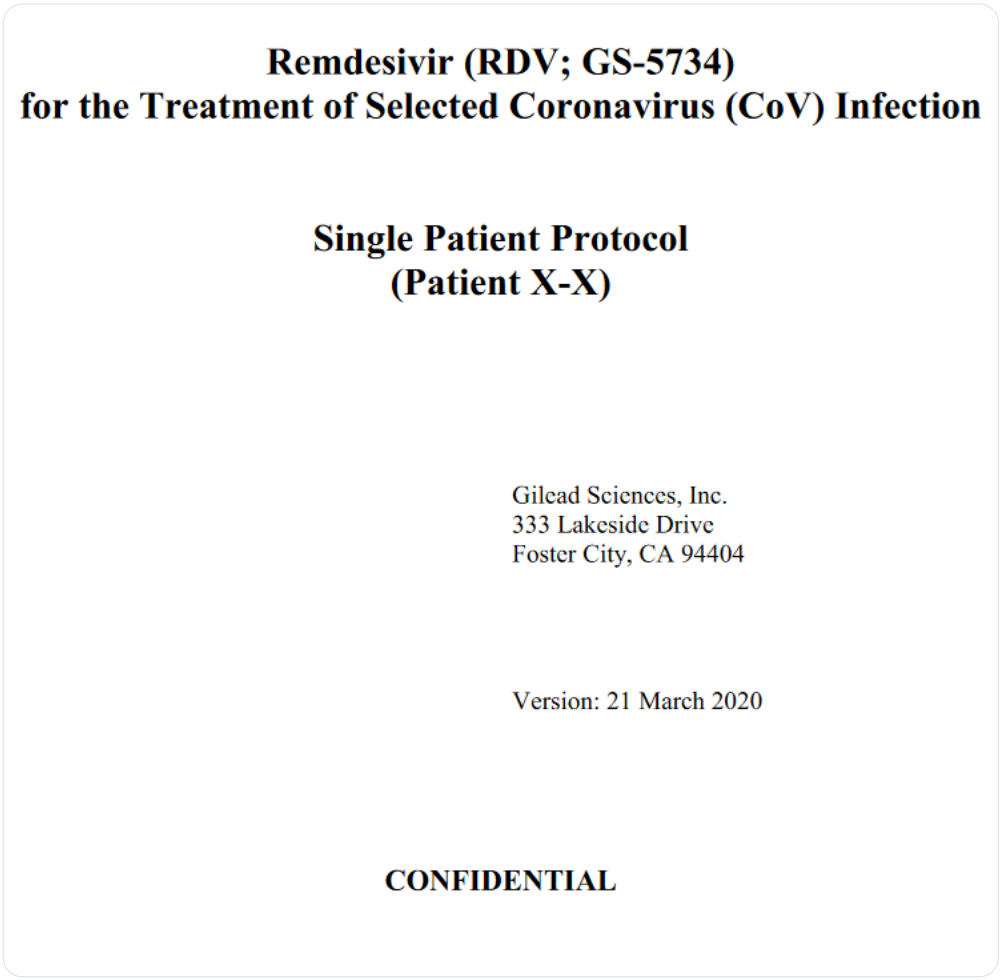
9🧵On page 73, virologist [not oncologist] Ralph Baric is awarded 11 grants totaling over $5.5m! 55% of which came by way of the NIAID & 36% came from Fauci's NIAID. The two most financed grants, each over $1million say so much about how they put the "plan" in "plandemic."



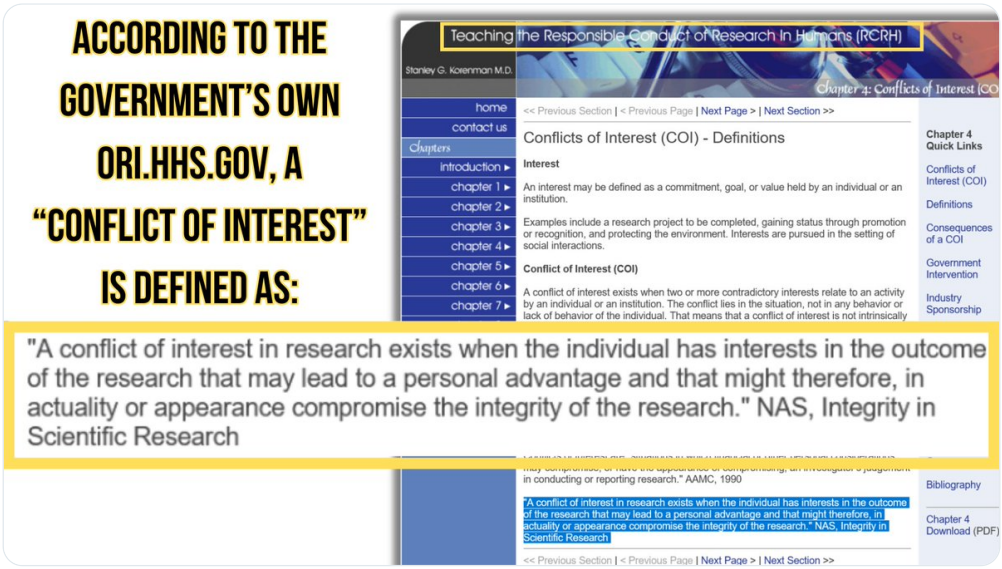


10🧵One grant for Baric was for looking into GS-5743 to "treat emerging coronaviruses" & the other million dollar grant was for "Respiratory Virus Vaccine & Adjuvants" Mind you, this is a 2019 report & GS-5743, btw, is the C19/Ebola poison, Remdesivir.





11🧵Lastly, I want to let the government & all implicated COVID criminals know that you guys are really good at playing the accidentally ignorant experts. You pretend your critics are conspiracy theorists but i know that YOU know the COIs/conspiracy plaguing you all. 👇U know!



12 🧾Receipts🔎

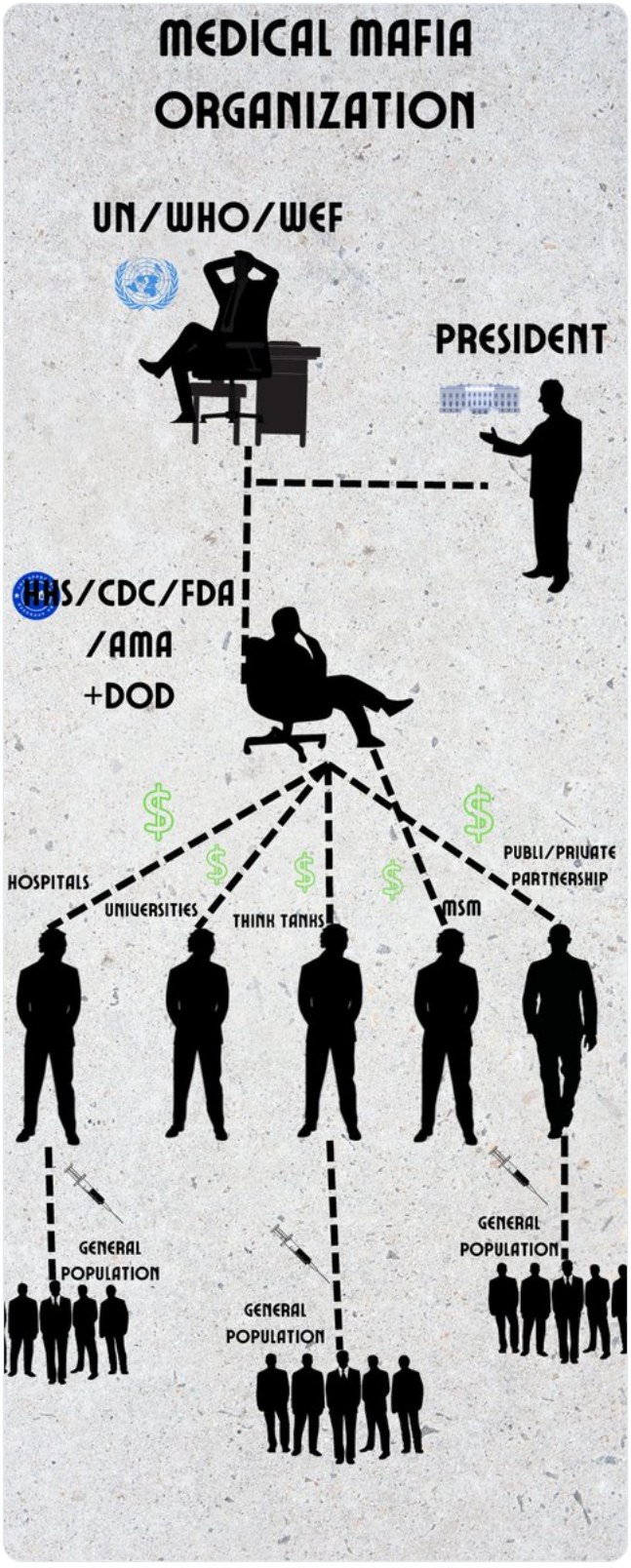
On behalf my friends, the vaccine injured: 🖕
You're gonna wish I took the jab, assholes. ✌️
I'm coming for the guilty. Bet on it. https://www.cancer.gov/research/key-initiatives/covid-19/serological-sciences-network/u54-centers-of-excellence
https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf
https://www.nejm.org/doi/suppl/10.1056/NEJMoa2007016/suppl_file/nejmoa2007016_protocol.pdf
https://www.thelancet.com/action/showPdf?pii=S0140-6736%2820%2930418-9

Sources:

https://thenewamerican.com/world-news/china/wuhan-lab-workers-wife-died-after-covid-like-flu-in-december-2019/
https://s3.documentcloud.org/documents/6935295/NIH-Moderna-Confidential-Agreements.pdf
https://www.pnas.org/doi/full/10.1073/pnas.1707304114 https://nihrecord.nih.gov/sites/recordNIH/files/pdf/2017/NIH-Record-2017-06-30.pdf https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf
https://osp.od.nih.gov/wp-content/uploads/NSABB_January_2020_Meeting_Minutes.pdf
https://reporter.nih.gov/search/vnX5NvoliUOlYqrHWmYq3g/publications https://www.cancer.gov/research/key-initiatives/covid-19/serological-sciences-network/u54-centers-of-excellence https://www.utmb.edu/gnl/news/2018/11/28/scientific-diplomacy-and-international-cooperation-key-say-bsl4-directors
https://www.nationalacademies.org/documents/embed/link/LF2255DA3DD1C41C0A42D3BEF0989ACAECE3053A6A9B/file/DC3F942EF28706DB42B20B193D5FDB0B799E795482C7?noSaveAs=1 https://reporter.nih.gov/search/wnpgFVi2PU2wIKH6zzFCog/projects
https://reporter.nih.gov/search/pOyEkDyRxkCzFMb_1ERKEQ/project-details/10688366
https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30418-9/fulltext
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf https://cdr.lib.unc.edu/downloads/zs25xd890
https://reporter.nih.gov/search/qkWL0AV0pUC-ztQD6umk-A/project-details/9328799 https://grantome.com/search?q=R01AI110700 https://www.nature.com/articles/s41579-018-0118-9 https://grantome.com/search?q=AI089728
https://pubmed.ncbi.nlm.nih.gov/27578435/
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf
https://reporter.nih.gov/search/qkWL0AV0pUC-ztQD6umk-A/project-details/9328799
https://pubmed.ncbi.nlm.nih.gov/28807998/ https://grantome.com/grant/NIH/R01-AI127521-01A1
https://patents.justia.com/patent/20200061185#history
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf
https://cdr.lib.unc.edu/downloads/zs25xd890 https://etd.ohiolink.edu/acprod/odb_etd/ws/send_file/send?accession=osu1681753185391367&disposition=inline https://www.biorxiv.org/content/10.1101/768663v1.full.pdf

My Sources?

https://usrtk.org/wp-content/uploads/2021/04/Saif-OSU-Batch-1.pdf
https://usrtk.org/wp-content/uploads/2022/12/UNC_Daszak-Media-Story.pdf
https://www.biorxiv.org/content/10.1101/768663v1.full.pdf
https://reliefweb.int/report/world/who-convened-global-study-origins-sars-cov-2-china-part-joint-who-china-study-14
https://www.who.int/publications/m/item/who-convened-global-study-of-the-origins-of-sars-cov-2
https://covid19.who.int/ https://ori.hhs.gov/education/products/ucla/chapter4/default.html
https://reporter.nih.gov/search/qkWL0AV0pUC-ztQD6umk-A/project-details/9328799 https://grantome.com/search?q=R01AI110700 https://www.nature.com/articles/s41579-018-0118-9
https://grantome.com/search?q=AI089728 https://pubmed.ncbi.nlm.nih.gov/27578435/
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf
https://reporter.nih.gov/search/qkWL0AV0pUC-ztQD6umk-A/project-details/9328799
https://pubmed.ncbi.nlm.nih.gov/28807998/ https://grantome.com/grant/NIH/R01-AI127521-01A1
https://patents.justia.com/patent/20200061185#history
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf
https://cdr.lib.unc.edu/downloads/zs25xd890 https://etd.ohiolink.edu/acprod/odb_etd/ws/send_file/send?accession=osu1681753185391367&disposition=inline
https://www.biorxiv.org/content/10.1101/768663v1.full.pdf https://www.science.org/doi/10.1126/scitranslmed.aal3653
https://journals.asm.org/doi/10.1128/jvi.03079-15
https://usrtk.org/wp-content/uploads/2022/12/UNC_Daszak-Media-Story.pdf
https://twitter.com/COVIDSelect/status/1730692429051826435



@threadreaderapp unroll

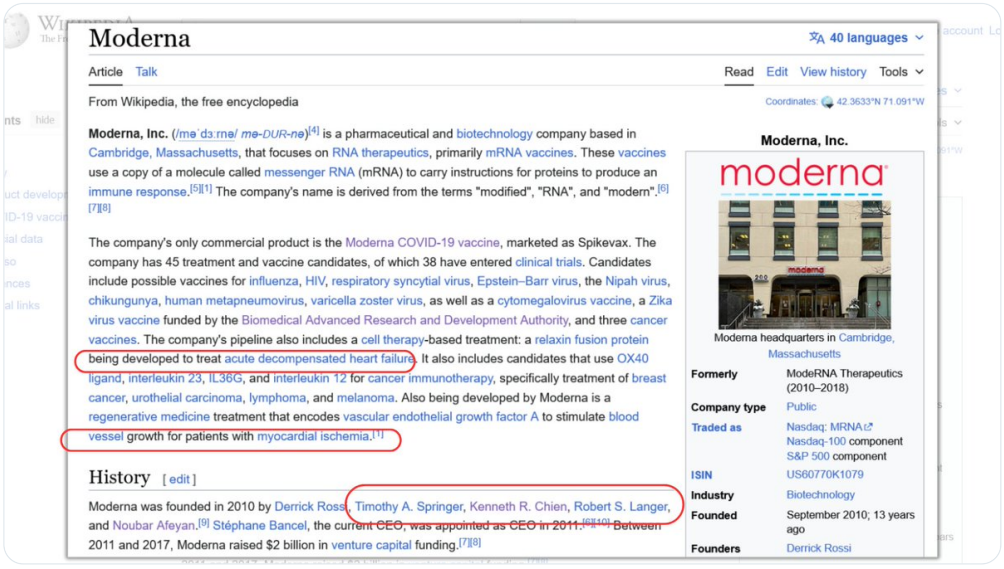
...

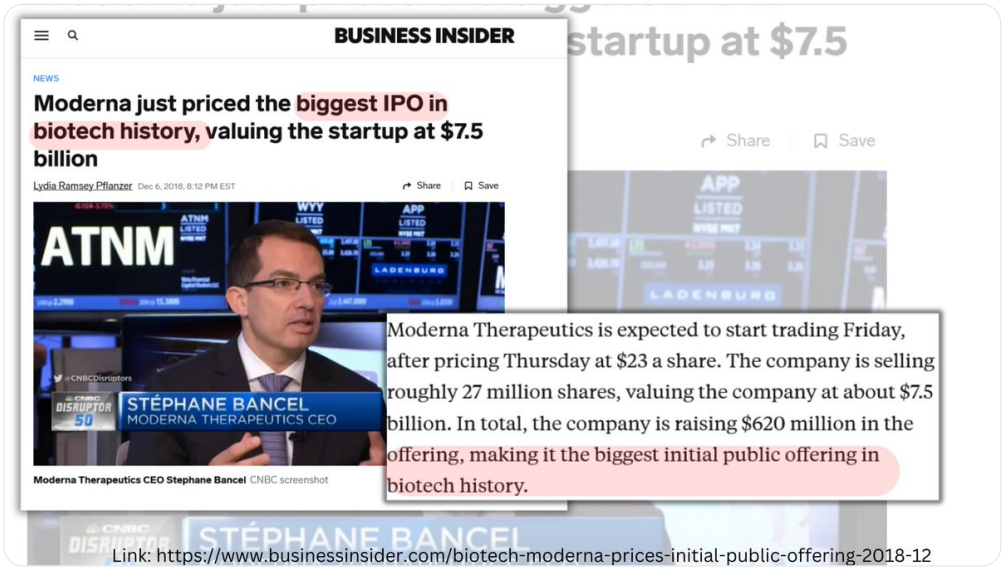
Destiny Rezendes @dezzie_rezzie

Feb 9, 2024 • 12 tweets • dezzie_rezzie/status/1756053850694287636

1🧵There is nothing that anyone can tell me to convince me that Ralph Baric of UNC Chapel Hill is an innocent character in the C19 Pandemic & neither is DARPA. By the end of this thread I'm sure you'll agree with me. [Buckle up, folks]

2🧵Let's start with Moderna, the company that Baric signed a Material Transfer Agreement [MTA] w/ in 2015, 2017, & 2019. Moderna had simultaneously signed a MTA with NIH's Vaccine Research Center [VRC] for mRNA CoV vaccine platform.





Link: https://www.businessinsider.com/biotech-moderna-prices-initial-public-offering-2018-12

3🧵 Now, Moderna was a new startup that prior to C19 hadn't brought a vaccine to market, they did however in 2013 joined DARPA for a $25M dollar project called ADEPT-PROTECT, whose stated goal is: Rapid development & deployment of medical countermeasures (MCMs) based on the encoding of antibodies in RNA and DNA. That's 25million of tax payer dollars to a company that had yet been successful by any meaningful measure. Moderna at the time was only 3 years old.

Product development [edit]

In 2013, the company formed a partnership with AstraZeneca to develop treatments for cardiovascular, metabolic, and renal diseases, as well as cancer. Moderna also was awarded a $25,000,000 grant by DARPA through a program Autonomous Diagnostics to Enable Prevention and Therapeutics: Prophylactic Options to Environmental and Contagious Threats (ADEPT-PROTECT).[11] Its stated goal was to develop an mRNA vaccine with the capability to suppress a global pandemic within 60 days. In January 2014, the company entered an agreement with Alexion Pharmaceuticals to develop treatments against ten diseases.[12] On January 14, 2014, Moderna announced the creation of its first venture, Onkaido Therapeutics, to focus "exclusively on developing mRNA-based oncology treatments."[13][14] It launched its second venture, Valera, in January 2015, with a focus on "viral, bacterial and parasitic infectious diseases."[15][16] Employees of Valera and Moderna developed an mRNA vaccine candidate against Zika virus infection.[17] Another venture, Elpidera, was announced in May 2015 to continue work on RNA therapies advancing Moderna's work with Alexion.[18][19]

In 2015, the company formed a partnership with Merck & Co. to develop treatments for cancer, and in 2016 the company formed a partnership with Vertex Pharmaceuticals to develop treatments for cystic fibrosis.[10][20][21][22] In January 2016, the Bill & Melinda Gates Foundation committed to provide at least $20 million in grant funding to the company.[1] In 2017, Alexion terminated its partnership with Moderna after safety issues prevented their work from reaching human trials.[23]

ADEPT : PROTECT

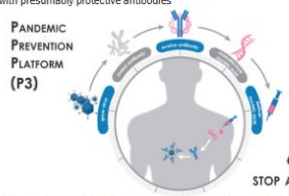
THE NEED AND OPPORTUNITY

A primary objective of DARPA's Biological Technologies Office (BTO) is to better ensure the health, and thereby the force readiness, of the country's military service community. The COVID-19 pandemic, which rapidly spread worldwide from an initial outbreak in China at the end of 2019, highlights one of the most perilous vulnerabilities to deployed military personnel and civilians: lack of protection and medical countermeasures (MCMs) against endemic and emerging biothreats. The Zika outbreak in 2015-2016, the more recent Ebola outbreak in the Democratic Republic of Congo, and mosquito-borne viruses such as Chikungunya and Dengue are among these threats.

Vaccines are the traditional mainstay of long-term infection prevention, while antibody approaches have at times been used to treat active infections. In one antibody-based approach that is being applied on a small scale in the current pandemic, blood serum with presumably protective antibodies obtained from those who have recovered from an infection is infused into patients. In more recent decades, monoclonal antibodies manufactured in cultured immune-system cells have been used to treat certain cancers and immune disorders. However, these treatments have suffered from shortcomings – including slow development, expensive manufacture, and dependence on continuous cold storage – that have prevented widespread use by the military.

THE DARPA SOLUTION

In 2012 with the ADEPT:PROTECT program*, DARPA began investing in the development of gene-encoded vaccines, a new category of preventive measures based on DNA or RNA. In this approach, genes that encode immune-stimulating antigens, such as the spike proteins on the surfaces of viruses like the one (SARS-CoV-2) that causes COVID-19, are delivered directly to a recipient's body. There, the instructions carried in the DNA or RNA elicit the body's own cells to manufacture the antigenic viral protein, which, in turn, elicits an immune response to the virus.



A follow-on effort to the ADEPT program, known as the Pandemic Prevention Platform program, aims to take pandemics off of the list of humanity's angsts with a range of technologies and practices marked by early detection of an outbreak and, within 60 days, development and widescale deployment of protective countermeasures.

Gene-based vaccines have shown great promise as a means to provide safe, reproducible, long-term immune protection. For vaccines to work, however, they often require more than one dose and it often takes weeks to months before a recipient's immune system builds up sufficient protection again the vaccine's viral target. With these biomedical realities come threats to warfighters if they deploy to pathogen-rife regions before having established relevant immunity and threats to military missions due to delayed deployment of personnel until they achieve immune protection.

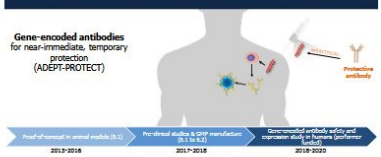
For a vaccine to confer immunity, it must lead to the production within a recipient of highly potent antibodies that can neutralize the pathogen. DARPA initiated the ADEPT:PROTECT program (most often referred to more simply as ADEPT) with the intention of bushwhacking a novel pathway to near-immediate protection against pathogens for which vaccines are not yet available and to confer interim-term protection during the development of a vaccine, which can take years.

THE IMPACT

DARPA's investments in this space led directly, with the biotechnology firm Moderna as a contracted performer on the program, to a first-ever human clinical trial with an RNA vaccine in 2019.

Earlier proof-of-concept experiments funded under ADEPT primarily with 6.1 funding (for basic research) demonstrated that delivery of antibody-making instructions – by way of messenger ribonucleic acid (mRNA), deoxyribonucleic acid (DNA), or another genetic-information-carrying tactic that relies on small viruses known as adenovirus-associated viruses (AAVs) – led to the production of antibodies that conferred protection in test animals exposed to the mosquito-borne Chikungunya (ChikV) virus.

DARPA pioneered the use of the body as a bioreactor to produce prophylactic antibodies to protect against biothreats



In a more applied phase of technology development, Moderna was converted to 6.2 funding (applied research) to begin pre-clinical studies in non-human primates with an RNA-encoded antibody against ChikV and to produce the countermeasure using Good Manufacturing Practices (GMP), which regulatory agencies such as the Food and Drug Administration often require.

Moderna subsequently used company funding to conduct a Phase I clinical trial with 22 healthy volunteers using an mRNA-encoded ChikV antibody. This marked the first safety demonstration of an RNA-based medical countermeasure. Moderna reported these promising results of its clinical study in 2019. The trial demonstrated platform safety as well as the ability to generate protective levels of functional antibody in humans. In response to COVID-19, Moderna in March 2020 initiated human trials of gene-encoded antibodies that target SARS-CoV-2.

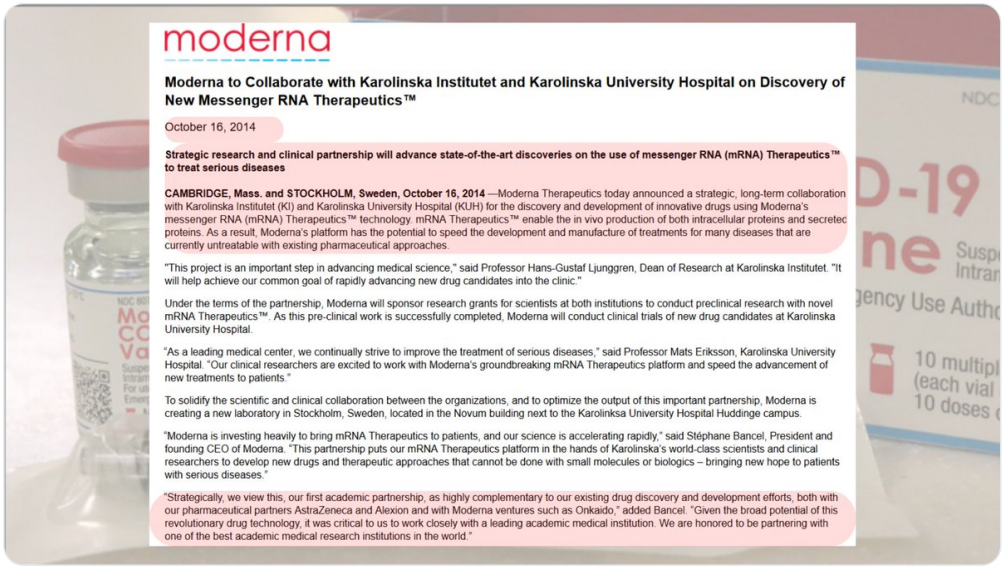
Research by Moderna and other ADEPT performers has provided proof-of-concept results that simultaneously delivering gene-encoded antibody treatment and vaccine confers the recipient with immediate immune protection while a long-term immune response develops.

LOOKING AHEAD

DARPA's R&D investments to de-risk the pathway to gene-based medical countermeasures have spurred like-minded innovators. In addition to Moderna, several other companies, including AstraZeneca and Inovio, have made major investments in this budding biomedical field. These DARPA investments also spurred the biotech firm RenBio to work toward optimizing the delivery of gene-based MCMs for increased efficacy and tolerability. Other government agencies – including the DoD's Joint Program Executive Office for Chemical, Biologic, Radiological, and Nuclear Defense (JPEO-CBRND), the Biomedical Advanced Research and Development Authority (BARDA), and the National Institute of Allergy and Infectious Disease (NIAID) – also have recognized the power of gene-encoded antibody technology to fight a range of biothreats and infectious diseases.

Progress in the ADEPT program has earned supplemental 6.2 funding from the U. S. Congress in response to the 2014 Ebola virus outbreak in West Africa. To address current and future Ebola outbreaks, these funds were directed toward development, manufacture, and/or clinical evaluation of several MCMs, including one

4🧵 One year later in 2014, Moderna lands a collaboration with the Karolinska Institute [KI] in Sweden. Important to note that one of their founders, Ken Chien was a research director at KI since 2013, his specialty was cardiovascular biotechnology. Just before Chien started at KI, he was approached by another Moderna Founder, Derrick Rossi to begin creating what would become Moderna. Chein's focus after that was focused on his studies that found "mRNA in heart muscle, resulting in a patent on the discovery that triggered mRNA towards therapeutic applications."


moderna

Moderna to Collaborate with Karolinska Institutet and Karolinska University Hospital on Discovery of New Messenger RNA Therapeutics™

October 16, 2014

Strategic research and clinical partnership will advance state-of-the-art discoveries on the use of messenger RNA (mRNA) Therapeutics™ to treat serious diseases

CAMBRIDGE, Mass. and STOCKHOLM, Sweden, October 16, 2014 —Moderna Therapeutics today announced a strategic, long-term collaboration with Karolinska Institutet (KI) and Karolinska University Hospital (KUH) for the discovery and development of innovative drugs using Moderna's messenger RNA (mRNA) Therapeutics™ technology. mRNA Therapeutics™ enable the in vivo production of both intracellular proteins and secreted proteins. As a result, Moderna's platform has the potential to speed the development and manufacture of treatments for many diseases that are currently untreatable with existing pharmaceutical approaches.

"This project is an important step in advancing medical science," said Professor Hans-Gustaf Ljunggren, Dean of Research at Karolinska Institutet. "It will help achieve our common goal of rapidly advancing new drug candidates into the clinic."

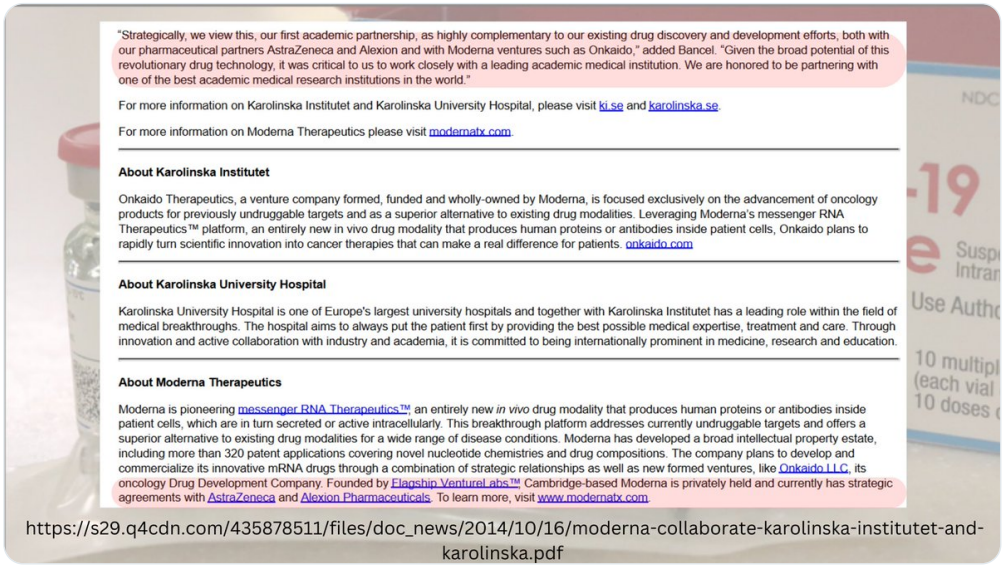
Under the terms of the partnership, Moderna will sponsor research grants for scientists at both institutions to conduct preclinical research with novel mRNA Therapeutics™. As this pre-clinical work is successfully completed, Moderna will conduct clinical trials of new drug candidates at Karolinska University Hospital.

"As a leading medical center, we continually strive to improve the treatment of serious diseases," said Professor Mats Eriksson, Karolinska University Hospital. "Our clinical researchers are excited to work with Moderna's groundbreaking mRNA Therapeutics platform and speed the advancement of new treatments to patients."

To solidify the scientific and clinical collaboration between the organizations, and to optimize the output of this important partnership, Moderna is creating a new laboratory in Stockholm, Sweden, located in the Novum building next to the Karolinksa University Hospital Huddinge campus.

"Moderna is investing heavily to bring mRNA Therapeutics to patients, and our science is accelerating rapidly," said Stéphane Bancel, President and founding CEO of Moderna. "This partnership puts our mRNA Therapeutics platform in the hands of Karolinska's world-class scientists and clinical researchers to develop new drugs and therapeutic approaches that cannot be done with small molecules or biologics – bringing new hope to patients with serious diseases."

"Strategically, we view this, our first academic partnership, as highly complementary to our existing drug discovery and development efforts, both with our pharmaceutical partners AstraZeneca and Alexion and with Moderna ventures such as Onkaido," added Bancel. "Given the broad potential of this revolutionary drug technology, it was critical to us to work closely with a leading academic medical institution. We are honored to be partnering with one of the best academic medical research institutions in the world."



"Strategically, we view this, our first academic partnership, as highly complementary to our existing drug discovery and development efforts, both with our pharmaceutical partners AstraZeneca and Alexion and with Moderna ventures such as Onkaido," added Bancel. "Given the broad potential of this revolutionary drug technology, it was critical to us to work closely with a leading academic medical institution. We are honored to be partnering with one of the best academic medical research institutions in the world."

For more information on Karolinska Institutet and Karolinska University Hospital, please visit ki.se and karolinska.se.

For more information on Moderna Therapeutics please visit modernatx.com.

About Karolinska Institutet

Onkaido Therapeutics, a venture company formed, funded and wholly-owned by Moderna, is focused exclusively on the advancement of oncology products for previously undruggable targets and as a superior alternative to existing drug modalities. Leveraging Moderna's messenger RNA Therapeutics™ platform, an entirely new in vivo drug modality that produces human proteins or antibodies inside patient cells, Onkaido plans to rapidly turn scientific innovation into cancer therapies that can make a real difference for patients. onkaido.com

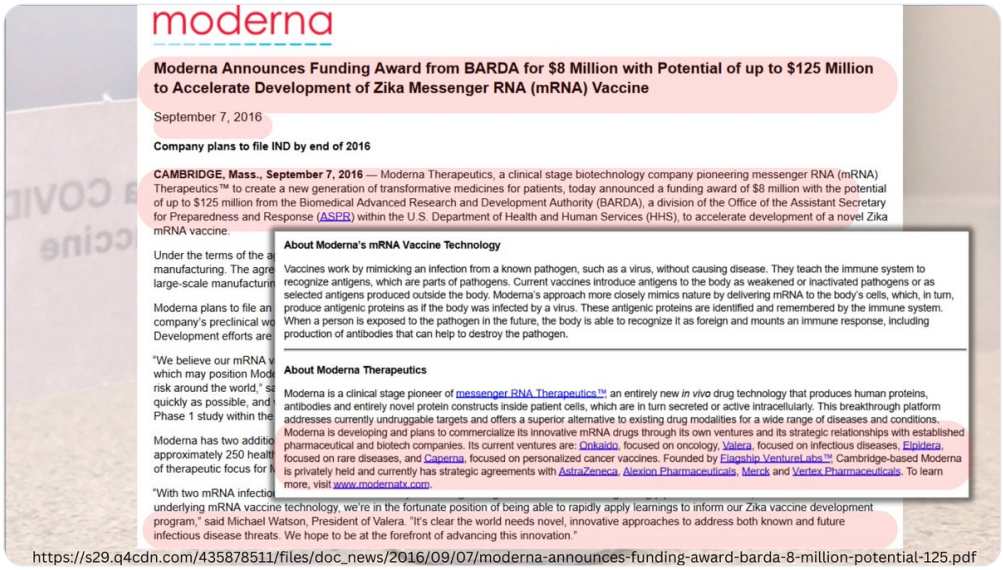
About Karolinska University Hospital

Karolinska University Hospital is one of Europe's largest university hospitals and together with Karolinska Institutet has a leading role within the field of medical breakthroughs. The hospital aims to always put the patient first by providing the best possible medical expertise, treatment and care. Through innovation and active collaboration with industry and academia, it is committed to being internationally prominent in medicine, research and education.

About Moderna Therapeutics

Moderna is pioneering messenger RNA Therapeutics™ an entirely new *in vivo* drug modality that produces human proteins or antibodies inside patient cells, which are in turn secreted or active intracellularly. This breakthrough platform addresses currently undruggable targets and offers a superior alternative to existing drug modalities for a wide range of disease conditions. Moderna has developed a broad intellectual property estate, including more than 320 patent applications covering novel nucleotide chemistries and drug compositions. The company plans to develop and commercialize its innovative mRNA drugs through a combination of strategic relationships as well as new formed ventures, like Onkaido LLC, its oncology Drug Development Company. Founded by Flagship VentureLabs™ Cambridge-based Moderna is privately held and currently has strategic agreements with AstraZeneca and Alexion Pharmaceuticals. To learn more, visit www.modernatx.com.

https://s29.q4cdn.com/435878511/files/doc_news/2014/10/16/moderna-collaborate-karolinska-institutet-and-karolinska.pdf



moderna

Moderna Announces Funding Award from BARDA for $8 Million with Potential of up to $125 Million to Accelerate Development of Zika Messenger RNA (mRNA) Vaccine

September 7, 2016

Company plans to file IND by end of 2016

CAMBRIDGE, Mass., September 7, 2016 — Moderna Therapeutics, a clinical stage biotechnology company pioneering messenger RNA (mRNA) Therapeutics™ to create a new generation of transformative medicines for patients, today announced a funding award of $8 million with the potential of up to $125 million from the Biomedical Advanced Research and Development Authority (BARDA), a division of the Office of the Assistant Secretary for Preparedness and Response (ASPR) within the U.S. Department of Health and Human Services (HHS), to accelerate development of a novel Zika mRNA vaccine.

Under the terms of the a
manufacturing. The agre
large-scale manufacturin

Moderna plans to file an
company's preclinical wo
Development efforts are

"We believe our mRNA v
which may position Mod
risk around the world," s
quickly as possible, and
Phase 1 study within the

Moderna has two additio
approximately 250 healt
of therapeutic focus for h

"With two mRNA infectio
underlying mRNA vaccine technology, we're in the fortunate position of being able to rapidly apply learnings to inform our Zika vaccine development program," said Michael Watson, President of Valera. "It's clear the world needs novel, innovative approaches to address both known and future infectious disease threats. We hope to be at the forefront of advancing this innovation."

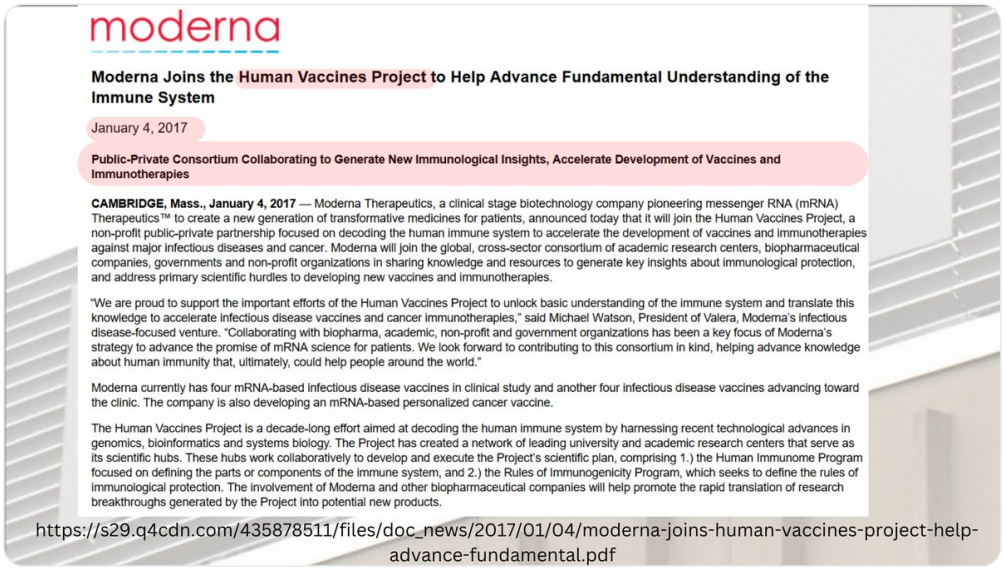
About Moderna's mRNA Vaccine Technology

Vaccines work by mimicking an infection from a known pathogen, such as a virus, without causing disease. They teach the immune system to recognize antigens, which are parts of pathogens. Current vaccines introduce antigens to the body as weakened or inactivated pathogens or as selected antigens produced outside the body. Moderna's approach more closely mimics nature by delivering mRNA to the body's cells, which, in turn, produce antigenic proteins as if the body was infected by a virus. These antigenic proteins are identified and remembered by the immune system. When a person is exposed to the pathogen in the future, the body is able to recognize it as foreign and mounts an immune response, including production of antibodies that can help to destroy the pathogen.

About Moderna Therapeutics

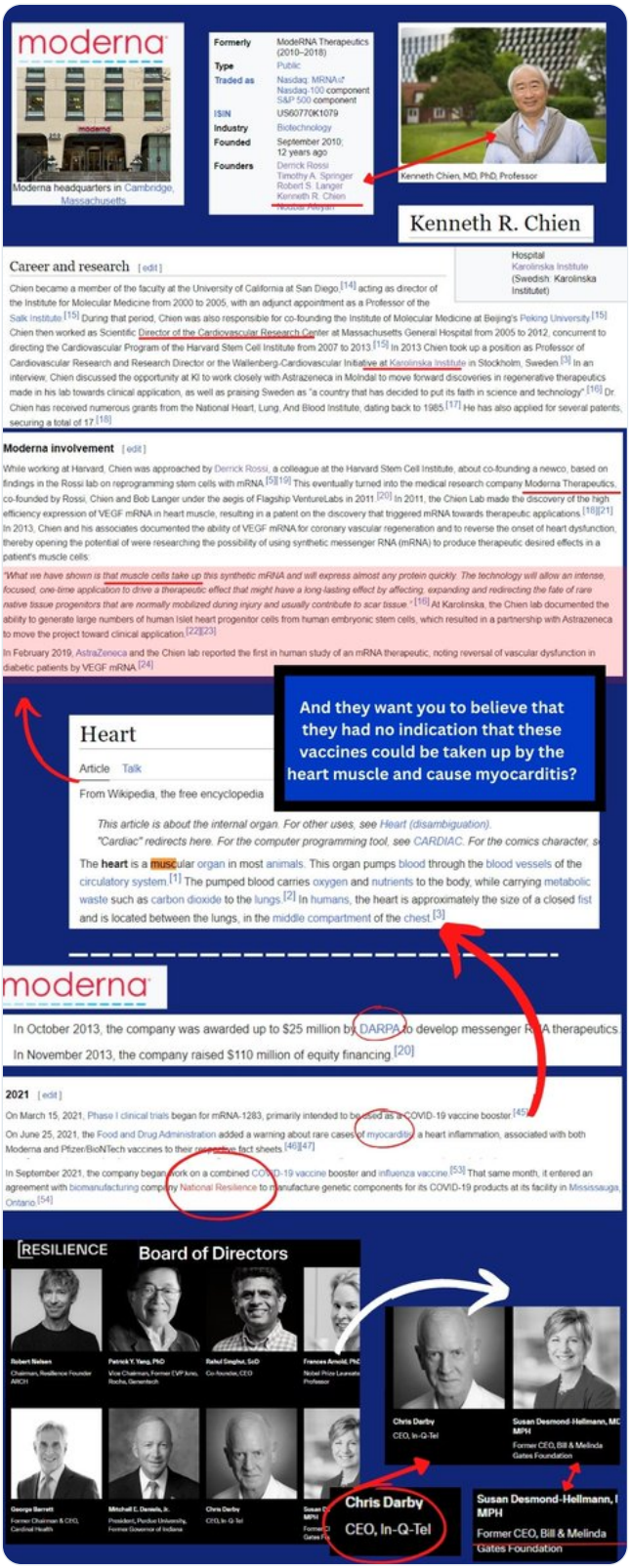
Moderna is a clinical stage pioneer of messenger RNA Therapeutics™ an entirely new *in vivo* drug technology that produces human proteins, antibodies and entirely novel protein constructs inside patient cells, which are in turn secreted or active intracellularly. This breakthrough platform addresses currently undruggable targets and offers a superior alternative to existing drug modalities for a wide range of diseases and conditions. Moderna is developing and plans to commercialize its innovative mRNA drugs through its own ventures and its strategic relationships with established pharmaceutical and biotech companies. Its current ventures are: Onkaido, focused on oncology, Valera, focused on infectious diseases, Elpidera, focused on rare diseases, and Caperna, focused on personalized cancer vaccines. Founded by Flagship VentureLabs™ Cambridge-based Moderna is privately held and currently has strategic agreements with AstraZeneca, Alexion Pharmaceuticals, Merck and Vertex Pharmaceuticals. To learn more, visit www.modernatx.com.

https://s29.q4cdn.com/435878511/files/doc_news/2016/09/07/moderna-announces-funding-award-barda-8-million-potential-125.pdf



https://s29.q4cdn.com/435878511/files/doc_news/2017/01/04/moderna-joins-human-vaccines-project-help-advance-fundamental.pdf

5🧵 Almost 2yrs ago I made this infographic to highlight these details. *As a side note; #BillGates the eugenics-minded college drop-out that pretends he's a doctor actually got a degree, albeit honorary, from the Karolinska Institute in 2004. https://www.fiercebiotech.com/biotech/press-release-bill-and-melinda-gates-to-receive-honorary-degrees-from-karolinska-institutet



6🧵 Where things get strange is when you find o/that BEFORE Baric started playing Frankenstein w/ Bat CoVs he was messing with Rabbit CoVs. In his 1992 publication Baric explored how Rabbit's infected w/CoVs suffered Myocarditis. Oddly its a similar mechanism to what Chien was looking into at KI when he started Moderna.

Pfizer

Science Products Stories Newsroom About

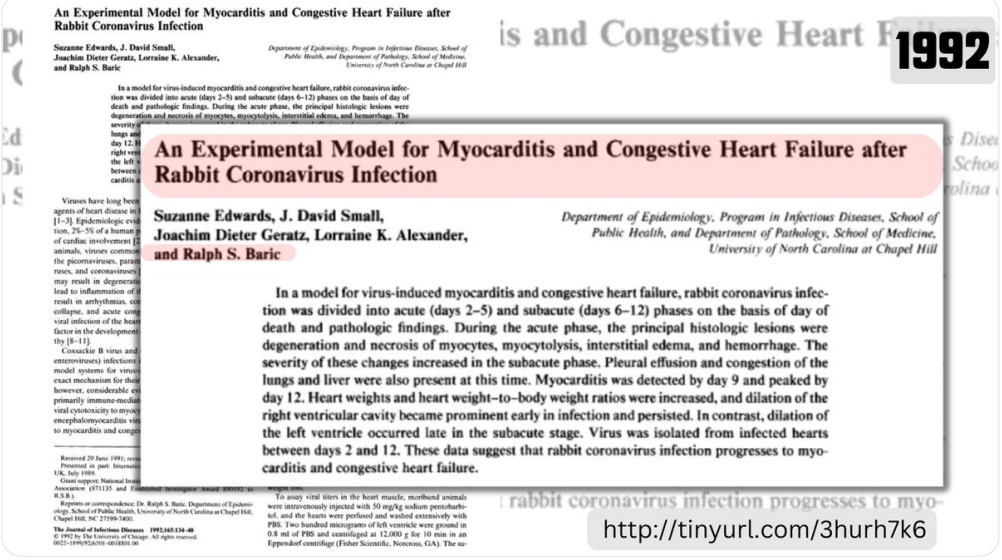
Pfizer Press release | Covid-19 | Vaccines

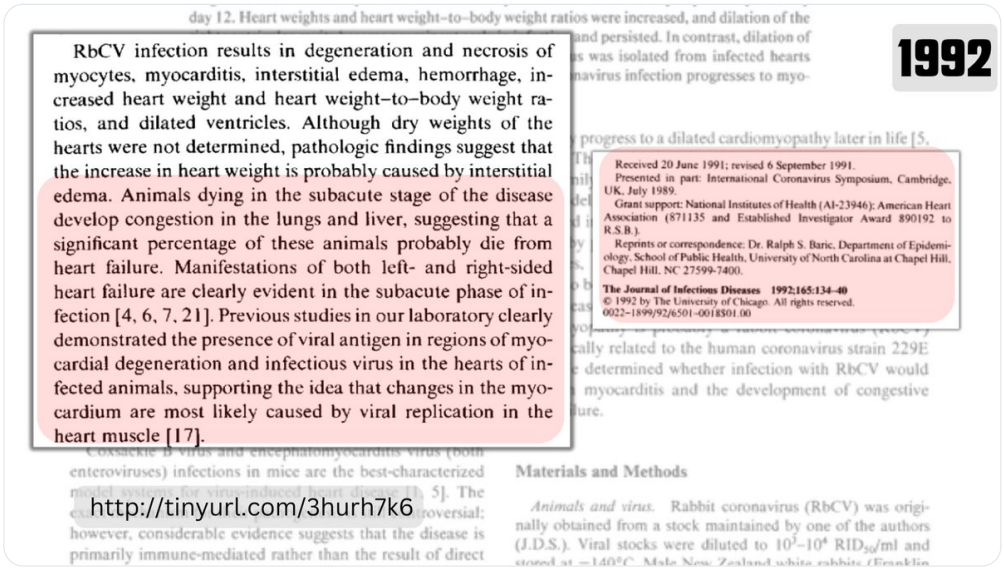
Pfizer and BioNTech Receive Expanded U.S. FDA Emergency Use Authorization of COVID-19 Vaccine Booster to Include Individuals 18 and Older

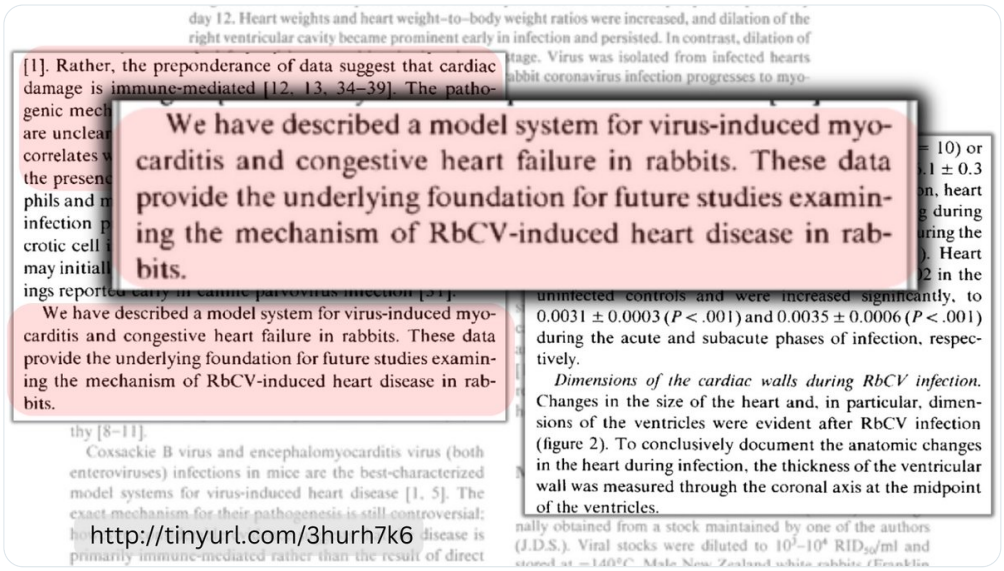
Friday, November 19, 2021 - 08:25am

- *Expanded authorization allows more Americans to receive a booster dose to help preserve a high-level of protection against COVID-19*

NEW YORK & MAINZ, Germany--(BUSINESS WIRE)-- Pfizer Inc. (NYSE: PFE) and BioNTech SE (Nasdaq: BNTX) today announced that the U.S. Food and Drug Administration (FDA) has expanded the emergency use authorization (EUA) of a booster dose of the Pfizer-BioNTech COVID-19 Vaccine to include individuals 18 years of age and older. The booster dose is to be







7🧵 We now know that Pfizer, who stole the mRNA C19 formula from Moderna, had known that Myocarditis was a Serious Adverse Event for their injections LONG before it was made public in November 2021 after it had been injected into billions of people. This has since been admitted by Pfizer & covered by great minds like @P_McCulloughMD & @JesslovesMJK

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10823859/

ECHOCARDIOGRAPHIC CHANGES FOLLOWING RABBIT CORONAVIRUS INFECTION

Lorraine K. Alexander, Bruce W. Keene, and Ralph S. Baric

The Department of Epidemiology
The University of North Carolina at Chapel Hill
Chapel Hill, North Carolina
The College of Veterinary Medicine
North Carolina State University
Raleigh, North Carolina

Much of our understanding of the mechanisms by which viruses cause myocarditis and/or dilated cardiomyopathy (DCM) is based on animal models of virus-induced heart disease. Information concerning cardiac function during acute and/or chronic viral infection in these models is limited (1). A well defined model in a species conducive to monitoring of cardiac function is needed to enhance our understanding of viral induced heart disease. We have previously demonstrated that rabbit coronavirus (RbCV) infection results in degeneration and necrosis of myocytes, myocarditis, and gross organ and histopathologic changes of DCM (2,3). We have also shown that electrocardiographic changes observed during RbCV infection mimic those in humans with myocarditis and DCM (submitted). This chapter describes the echocardiographic changes observed during RbCV infection.

Eleven male New Zealand white rabbits were sedated prior to echocardiography with a combination of xylazine (0.17 mg/kg) and ketamine (17 mg/kg). An electrocardiogram was monitored continuously during echocardiography and two-dimensional echocardiographic views were recorded with the animal in right lateral recumbancy from the right parasternal long and short-axis positions using a 7.5 MHz annular array transducer. Measurements of left ventricular (LV) size, systolic function, mitral valve motion, and aortic and left atrial diameter were made according to the American Society of Echocardiography standards for M-mode echocardiography. Briefly, M-mode measurements included LV end diastolic and systolic chamber dimensions and wall thickness obtained by guiding the M-mode cursor between the papillary muscles from a right parasternal short-axis imaging plane just ventral to the mitral valve leaflets at the level of the chordae tendinae. Aortic and left atrial dimensions were measured from an M-mode view obtained by guiding the cursor through the aorta and left atrium in a right parasternal short short axis view at the level of the aortic valve. The mitral valve motion and E-point - septal separation was observed and recorded from M-mode images obtained by guiding the cursor through a right parasternal

Corona- and Related Viruses, Edited by P. J. Talbot and G. A. Levy

Table 1. Cardiac function values for 11 RbCV infected rabbits

Measurement	Uninfected[a] n = 11	Nonsurvivor[a,b] n= 6	Survivor[a,b] n= 5
Left Ventricular (LV) diameter (d)[c] (cm)	1.42 ± 0.24	1.13 ± 0.44	1.14 ± 0.12
LV diameter (s)[d] (cm)	0.92 ± 0.17	0.93 ± 0.38	0.84 ± 0.17
% fractional shortening	35.5 ± 4.85	17.33 ± 6.19	26.17 ± 12
Septal wall thickness (d) (cm)	0.22 ± 0.07	0.25 ± 0.06	0.22 ± 0.05
Septal wall thickness (s) (cm)	0.38 ± 0.08	0.28 ± 0.09	0.33 ± 0.12
LV posterior wall thickness (d) (cm)	0.31 ± 0.11	0.32 ± 0.08	0.26 ± 0.03
LV posterior wall thickness (s) (cm)	0.50 ± 0.12	0.44 ± 0.13	0.42 ± 0.06
Left atrium diamter (cm)	0.88 ± 0.14	0.93 ± 0.15	0.86 ± 0.10
Aorta (cm)	0.66 ± 0.12	0.74 ± 0.13	0.68 ± 0.05
Left atrium/Ao	1.22 ± 0.20	1.36 ± 0.29	1.28 ± 0.14
E-point septal separation (EPSS)	0.14 ± 0.04	0.22 ± 0.16	0.126± 0.09

a = Mean ± SD.
b = Day 3 after infection.
c = diastole.
d = systole.

short axis view at the level of the mitral valve. LV fractional shortening was calculated as an ejection phase index of systolic function. All values reported reflect the mean of 3 measurements made on sinus beats. Rabbits were infected with 0.3 ml of a 1X 10^3 - 1X 10^4 RID_{50} of RbCV and echocardiographic measurements were repeated using the same anesthetic and measurement protocol on days 3, 6, 9, 12 and 30 post-infection.

Two (18%) rabbits died during the acute phase of infection (day 3), 4 (36%) died in the early subacute phase (day 6), and 5 (46%) survived beyond day 12 into the chronic phase. Echocardiographic data is displayed in Table 1. The index of systolic ventricular function

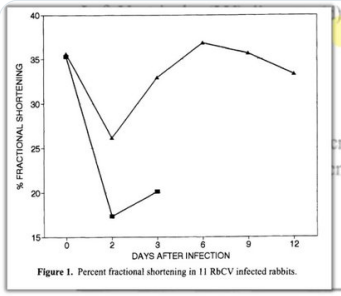
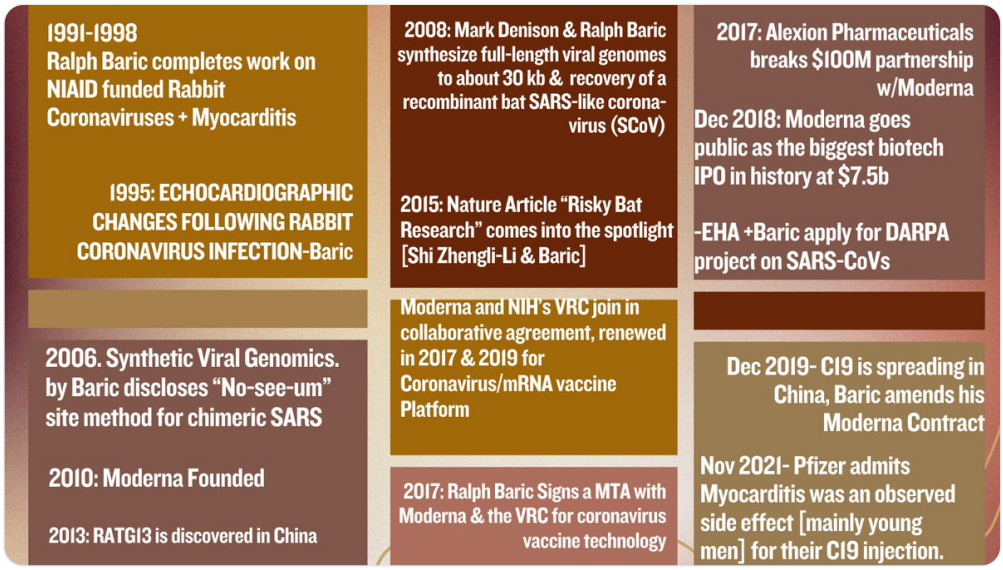


Figure 1. Percent fractional shortening in 11 RbCV infected rabbits.

chosen, % fractional shortening was depressed in all infected rabbits by day 3 post infection (Figure 1). Fractional shortening was more depressed in nonsurvivors (17.33 ± 6.19%, p= <.001 from controls) as compared to survivors (26.17 ± 12%, ns from control). Mean LV wall thickness, chamber dimensions, and left atrial dimensions were not significantly different from controls throughout the study in either survivors or nonsurvivors. These findings confirm our previous pathologic studies in which rabbits dying early in infection (days 2-5) did not have significantly different LV wall thickness, and chamber dimensions from control animals.

We conclude that RbCV infection depresses an ejection phase index of systolic LV function, that this depression precedes gross morphologic changes in the ventricle, and that severe systolic dysfunction correlates positively with mortality. These findings provide a direct link between the severity of virus-induced cardiac dysfunction and survival during RbCV infection, characterizing a reproducible model of cardiac dysfunction following viral infection of the heart.

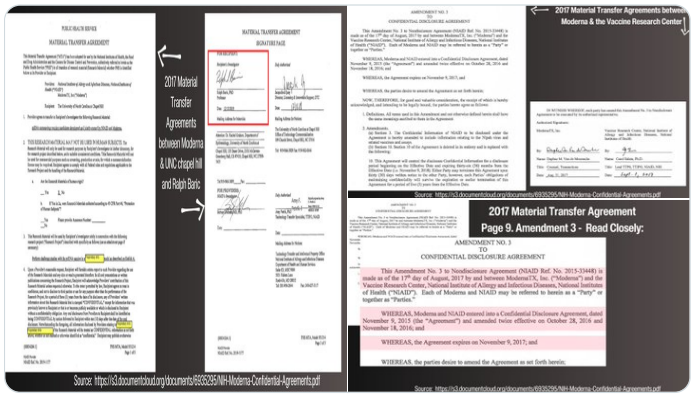


8🧵This thread is already not for the faint of heart, so to save time I suggest reading the details of the MTA between Moderna, Baric and the NIH's VRC leading up to 2020: & how Moderna made the C19 jab formulation in ONE DAY:

Destiny Rezendes
@dezzie_rezzie · **Follow**

Replying to @dezzie_rezzie

8🧵In that same MTA, later amended, Ralph Baric signs the MTA in 2019 for the same technology but read Amendment 3 carefully. According to the contract, the collaboration between VRC and Moderna didn't start in 2017, but rather on Nov 9, 2015.🔎🤫



10:45 PM · Nov 30, 2023

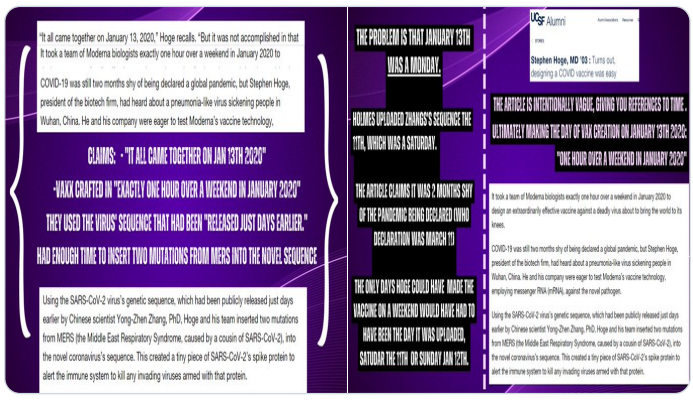
72 See the latest COVID-19 information on X

Read 2 replies

Destiny Rezendes
@dezzie_rezzie · **Follow**

Replying to @dezzie_rezzie

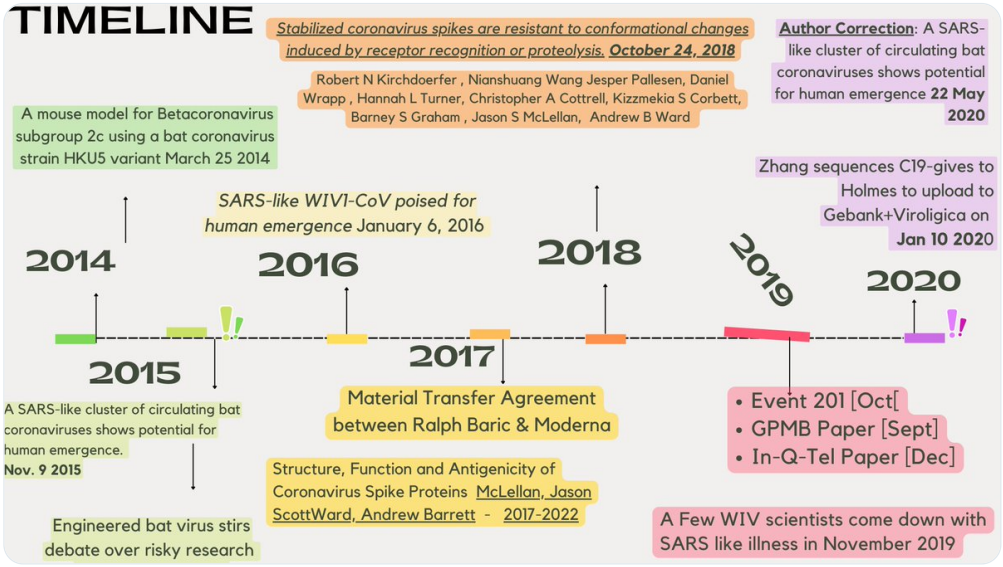
10🧵Hoge (Moderna) claims he created the C19 💉in 1hr, over a weekend on Jan 13th 2020. However, the 13th was a weekday- a Monday. Zhang/Howell uploaded the sequence on Sat. the 11th. Hoge admits he was "Eager" to get to "Test" out the 💉.



6:14 AM · Mar 20, 2023

20 See the latest COVID-19 information on X

Read 3 replies



JOURNAL ARTICLE

An Experimental Model for Myocarditis and Congestive Heart Failure after Rabbit Coronavirus Infection

Suzanne Edwards, J. David Small, Joachim Dieter Geratz, Lorraine K. Alexander and Ralph S. Baric

The Journal of Infectious Diseases

Vol. 165, No. 1 (Jan., 1992), pp. 134-140 (7 pages)

Published By: Oxford University Press

About the Human Vaccines Project

The Human Vaccines Project is a non-profit public-private partnership with the mission to accelerate the development of vaccines and immunotherapies against major infectious diseases and cancers by decoding the human immune system. The Project has a growing list of partners and financial supporters including: Vanderbilt University Medical Center, the J. Craig Venter Institute, the La Jolla Institute, The Scripps Research Institute, UC San Diego, Aeras, Boehringer Ingelheim, Crucell/Janssen, GSK, Pfizer, MedImmune, Regeneron, Sanofi Pasteur, the Robert Wood Johnson Foundation and the John D. and Catherine T. MacArthur Foundation. The Project brings together leading academic research centers, industrial partners, nonprofits and governments to address the primary scientific barriers to developing new vaccines and immunotherapies, and has been endorsed by 35 of the world's leading vaccine scientists. www.humanvaccinesproject.org

---

About Moderna Therapeutics

Moderna is a clinical stage pioneer of messenger RNA Therapeutics™; an entirely new in vivo drug technology that directs the body's cells to produces human proteins, antibodies and entirely novel protein constructs, which are in turn secreted or active intracellularly. With its breakthrough platform, Moderna is developing mRNA vaccines and therapeutics to address currently undruggable targets and deliver a new class of medicines for a wide range of diseases and conditions. Moderna is developing and plans to commercialize its innovative mRNA medicines for infectious diseases, cancer (immunooncology), rare diseases, cardiovascular disease and pulmonary disease, through its ecosystem of internal ventures and strategic partners.

Headquartered in Cambridge, Mass., privately held Moderna currently has strategic agreements with AstraZeneca, Merck, Alexion Pharmaceuticals and Vertex Pharmaceuticals, as well as the Defense Advanced Research Projects Agency (DARPA), an agency of the U.S. Department of Defense; the Biomedical Advanced Research and Development Authority (BARDA), a division of the Office of the Assistant Secretary for Preparedness and Response (ASPR) within the U.S. Department of Health and Human Services (HHS); and the Bill & Melinda Gates Foundation. To learn more, visit www.modernatx.com.

Moderna Contacts:

Investors:
Maren Winnick
617-674-5297

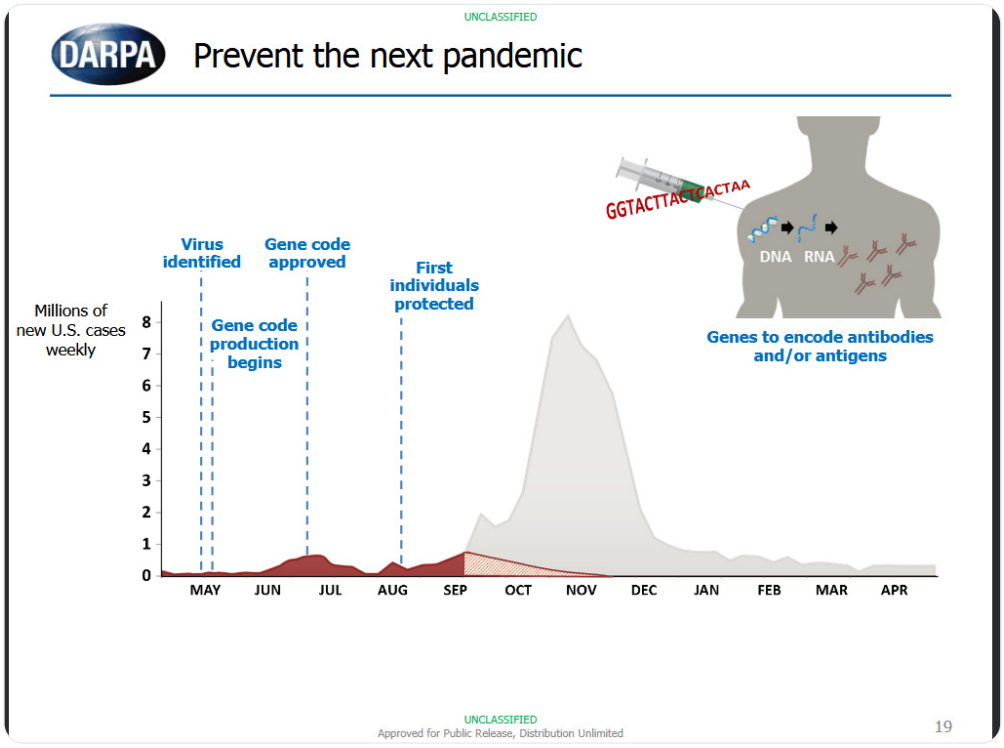
9🧵What's the tie? DARPA's wishes of Synthetic Biology and Rapid Countermeasure deployments who outside of the DEFUSE project was ALREADY working with Moderna who was ALREADY working with Ralph Baric before the pandemic started! You'll see this truth in DARPA's internal document [unclassified] from 2017👇

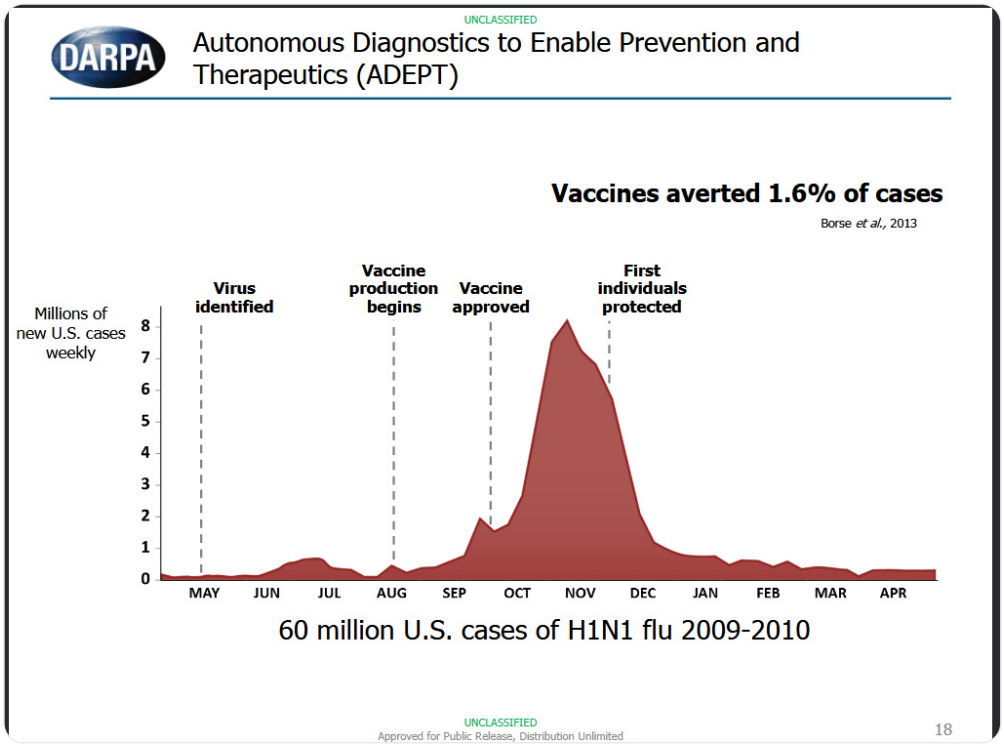
Defense Advanced Research Projects Agency

Stefanie Tompkins, Ph.D.
Acting Deputy Director

NDIA S&ET Conference

April 18, 2017





10🧵 The reality is DARPA didn't approve the DEFUSE project likely because they realized they didn't need EHA to move forward w/their goals. Eco Health was already deep in w/ USAID [CIA front] & according to Chris Darby of In-Q-Tel in 2019, the intelligence community's top focus was bio-data.

-Eco Health was successful in its role with USAID in China and SE Asia & ADEPT was already making great strides, as was Moderna & Baric.

-So, Baric knew since the 1990's that CoV's could cause Myocarditis in infected mammals that was similar to its presentation in humans.

-The scientific community knew since 2003/4 that SARS vaccines were largely ineffective and that the spike protein and mRNA bio-accumulated in vital organs, like the heart.

-The US's biological research oversight group, the NSABB, knew since 2006/7 that Baric could create a full CoV genome WITHOUT leaving a trace that it was lab altered & NIH knew [because they funded it] that Baric was doing GOF research with Corona-Virologists in Wuhan and w/ EHA.

-The USG KNEW since 2018/2019 that Wuhan Institute of Virology was lacking in their safety regulations [despite being trained by University of TX Medical Branch staff] and they knew the science was ongoing regardless.

-HHS knew that Baric led the forefront on not only the vaccine [Moderna] but also the heavily pushed his Monoclonal antibody "treatment" Remdesivir, which is a FAILED Hept/Ebola/Zika "treatment" and the men who helped him; Mark Denison & Barney Graham all received MILLIONS after the "vaccine rollout" allotted to their establishments for intellectual property rights [Vanderbilt Univ, Vaccine Research Center/NIH]

AND YET... The Peter Daszak Transcript from NOV 2023 has not been released! The recent Fauci transcript has YET TO BE RELEASED. AND RALPH BARIC HAS NEVER HAD TO BE HELD ACCOUNTABLE or properly investigated over C19!

The USG put 5 TRILLION DOLLARS into a "Pandemic Oversight Fund" [the largest financial effort in mankind's history] but they can't afford to investigate this pandemic or vaccine which has Injured and killed people all over the world.

What about those who lost their kids to Myocarditis post vaccination?! You're gonna tell them its all a coincidence and it was "for the greater good?"

Despite what CCN medical correspondent, & freedom-hater, Dr. Leana Wen thinks, WE ARE NOT RABBITS. We are humans who deserve the truth & I shouldn't have to throw my life away to learn all this crap!

I'm not apologizing for the long post- You don't like it then do it yourself. Otherwise, links will be added [if not already on the slides] as a comment to avoid algorithm throttling.

SOURCES

https://s29.q4cdn.com/435878511/files/doc_news/2016/09/07/moderna-announces-funding-award-barda-8-million-potential-125.pdf

https://s29.q4cdn.com/435878511/files/doc_news/2017/01/04/moderna-joins-human-vaccines-project-help-advance-fundamental.pdf

http://tinyurl.com/3hurh7k6

https://www.statnews.com/2017/01/10/moderna-trouble-mrna/

https://s29.q4cdn.com/435878511/files/doc_news/2014/10/16/moderna-collaborate-karolinska-institutet-and-karolinska.pdf

https://www.forbes.com/sites/nathanvardi/2016/12/14/modernas-mysterious-medicines/?sh=e551f1c6ef6f

https://watermark.silverchair.com/165-1-134.pdf?token=AQECAHi208BE49Ooan9kkhW_Ercy7Dm3ZL_9Cf3qfKAc485ysgAAA1QwggNQBgkqhkiG9w0BBwagggNBMIIDPQIBADCCAzYGCSqGSIb3DQEHATAeBglghkgBZQMEAS4wEQQMefFJyy5N34yKfyeNAgEQgIIDB7HpExDF6lU6WCmtxSDszhkycfx1dsHvbpx0DTrqtNSQtefJ_H_be-JUoCqoXpbqcPp7Go4QZ7dJ72jGtI56376v__5JYujjGnebbciw8Dke--IZ-oa1DWV9KUv2tR32v5t9-SiZDqmQbv0rNIdVf2UqVc9fS6CRyXktCgby9WrxT1eh3VmV9qVHFm_rriCtN7WsvfACnswvmWPLi-cYI5CbLJ2ayrVs3Ivi5p23vv_vK5nHWGdCBiZ2ERq1NtzxBCdXB5nDUwRnuUVyTLJr1T4y21WccuClb5IixjDvRTM3HrOWLtkJ4cdfdprHcHHuxISRrGhoZbNLPfM22NwYY6yS6XZe5nKJGFeN2KsGiHm3CbsXlquewAj7nMibPq6ca9MTluCORhooJ8HuBTH6BzdUhCU19eil49NUYhhNsOGaTbY5Zv4CpOk3t2bz7bPNUFBi6AVHzKd93ZM8SkP6LMVXTFwtOJEMowXrAgfGML4uqKche9SKRlEPfmJbXKhYQ6Vv7twq29vS0nNbWUs6X7kAKhkUPu8Pop3Kb0Ajixa05N2GvxrU4isvwuNxAWiyUQvihQ310MbbrQBap0TDUHemkysH0DoGWbdK-4ONV7lcDtExVJFcfObkYYj01k8iG0Mzg88DCb0kkdMrtF9skpiZS8aO_i80PDJwoNJN1Zbh0VwBfbradAHa58-_mGT78YuzB--X94sy7rY8yJtu1ozzdb2GmE7tBj8znXSXC1JUGI5vdf1ZU3cLe1_DTWIAFWJ8-07Ouej5yF0O4jnjlDTF3Csu7ztXjB6h_4VxRxJeFb1jCB5QmPFIebJRKvtKiZQCrd9mc4sbjkaTBh5yqcSvkpgiWd_Bkx7WiO8kH2UPupiWlx_Ef2FBNeoxCqYxTVfVAQvvLln1kfJrcEyjlD1_ghfahAlvpu5eWBeldz0PbxCybTog9YI4gFiEyJwlpTjW-YLhqAjC8BwAM-q9Ji7GBF93yR-_bIAO0RFmEK07-7ToaDyoKBHaMkJvKOR9fMRqmiKbL8

https://link.springer.com/content/pdf/10.1007/978-1-4615-1899-0_18.pdf

More Links:
Gates Karolinska 2014:

Pubmed Myocarditis Eval 2022:

DARPA 2017/ADEPT program Unclassified:

Moderna on mRNA +DARPA from 2018 Internal Doc pg 27-57:

Moderna's beginnings 2017 article:

ADEPT-Protect:

Jessica Rose & @P_McCulloughMD 's Jan 2024 paper on Vaccine induced Myocarditis 🔥:

1995 Baric article:ECHOCARDIOGRAPHIC CHANGES
FOLLOWING RABBIT CORONAVIRUS INFECTION

Baric article on CoV induced Myocarditis in Rabbits:

Archive of Pfizer's release statement on Myocarditis:

All other used references are in the Sources Image at the end of the thread. Thank you and God Blesshttps://www.fiercebiotech.com/biotech/press-release-bill-and-melinda-gates-to-receive-honorary-degrees-from-karolinska-institutet
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9130641/
https://ndiastorage.blob.core.usgovcloudapi.net/ndia/2017/science/Tompkins.pdf
https://s29.q4cdn.com/435878511/files/doc_financials/2018/ar/Chasen-Richter-Moderna-Annual-Report-2018.pdf

Key partner cuts ties with brash biotech startup Moderna, raising big ...
Moderna Therapeutics, a $5 billion startup that boasts of changing the world, is losing a key partner, imperiling its most advanced drug project.
https://www.statnews.com/2017/07/27/moderna-alexion-partnership/

https://www.federalgrants.com/Autonomous-Diagnostics-to-Enable-Prevention-and-Therapeutics-Prophylactic-Options-to-Environmental-and-Contagious-Threats-ADEPT-PROTECT-38431.html
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10823859/
https://link.springer.com/content/pdf/10.1007/978-1-4615-1899-0_18.pdf
jstor.org/stable/30112503
https://web.archive.org/web/20231207023910/https://www.pfizer.com/news/press-release/press-release-detail/pfizer-and-biontech-receive-expanded-us-fda-emergency-use
@Bryce_Nickels @emilyakopp @WashburneAlex @VigilantFox @TTAVOfficial @SenRonJohnson @COVIDSelect @NIH @AGHuff

• • •